

INFORMAL SEQUENCE LISTING

SEQ ID NO:1

5 ABC Transporter
GL2_96_2C01_G3F1
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SEQ ID NO:2

20 ABC transporter>
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SEQ ID NO:3

>gi|7262392|ref|NM_000033.2| Homo sapiens ATP-binding cassette, sub-family
 D (ALD), member 1 (ABCD1), mRNA

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SEQ ID NO:4

>gi|7262393|ref|NP_000024.2| ATP-binding cassette, sub-family D (ALD),
 member 1; adrenoleukodystrophy protein [Homo sapiens]
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 40 YMHSRVVANSEIEAFYGGHEVELALLQRSYQDLASQINLILLERLWYVMLEQFLMKYVWSASGLLMVAVP
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 45 CTSVAVSIDVEGKIFQAADAGIALLSITHRPSLWKYHTHLLQFDGEGGWKFEKLDAAARLSLTEEKQRL
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SEQ ID NO:5

PCBP1
 GL2_131_2_M13F
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SEQ ID NO:6

GL2-77-2M13R
 60 CGCTGCGGCCTCCCGCCCGCTCCCGCTCGCTCCCGCGGCCTCGCTCGCCTCGCGCCGGCAGTTTTGGGCCCTACAC
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SEQ ID NO:7

GL2_209_3_M13R

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SEQ ID NO:8

GL2_131_3_M13F

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SEQ ID NO:9

GL2_205_C05_G3F1

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SEQ ID NO:10

GL2_131_3_M13R

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SEQ ID NO:11

GL2_209_1_M13R

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SEQ ID NO:12

GL2_131_2_M13R

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SEQ ID NO:13

GL2_81_1_M13F

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SEQ ID NO:14

GL2_77_1_M13F

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SEQ ID NO:15

GL2_77_1_M13R

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SEQ ID NO:16

GL2_77_2_M13F

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SEQ ID NO:17

GL2_77_3_M13F

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SEQ ID NO:18

GL2_77_4_M13F

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TTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCAC
GCCAGCGATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCCACCTGGACCTGCGCCCCCGTACT
CTCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCT
CAGGGTGACCGGGGGCCTGCTGGCCCGGTAAGTCTGGTTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTTCGAT
GATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGGACAATTCCCCTC
CGAGATGTTGATCCGCGCGCCACTCTCCTCGCGGATCCTCT

SEQ ID NO:19

GL2_77_5_M13F

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
ACCGATCTTGGCCGCCCGCGCAGATACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCCC
TTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCAC
GCCAGCGATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCCACCTGGACCTGCGCCCCCGTACT
CTCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCT
CAGGGTGACCGGGGGCCTGCTGGCCCGGTAAGTCTGGTTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTTCGAT
GATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGGACAATTCCCCTC
CGAGATGTTGATCCGCGCGCCACTCTCCTCGCGGATCCTCTTAAACCGACTCCCCTTTCTTCCCAAATGATGCTTC
CTACTTCCCTTTTCCGTGCATAAGAAAGCCGAAATGGTGAGAG

SEQ ID NO:20

GL2_131_1_M13F

NNGCTGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACATCATGACCGGCCCCACCAATGCCA
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GGCACAGCAGGCCCCACGGGTACCCCTGAGGCTGGATGGTGCCGGCCACCCAGATGCGGCTCCCTGATANGGGAA
AGGCGGGTGTAAGATCAAAGAGATCANNAGAGAGTACGGGNGCGCAGGTCCAAGGAATGGCAGGAGGGATATGC
ATGCCCAAAAACAACCGAGACGGGCCAAANACCATAGCTGGACAGTGCCGAAGGACTGTCACCNGAAGAT

SEQ ID NO:21

GL2_131_1_M13R

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
ACCGATCTTGGCCGCCCGCGCAGATGACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCC
CTTGCGGGAGAACTGGGGAAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGC
GGCACGCCAGCAATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCCACCTGGACCTGCGCCCCC
GTACTCTCGCGGATCTCTT

SEQ ID NO:22

GL2_209_2_M13R

GGCGCCAGTGCTGCTGCNATTGCGNTATCTCTCGGCATGGACGAGCTGGTACAAAAAGGAGGAGGGCCCGCAAGTC
GGTGGCAGCGGTGGCTCCAGTGTTGGCTGGGGGGGTTCTGCGGCTTGAATCGGAAGGTTAAGGGGGCATCCAGA
GGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGCACCGATCTTGGCGCCGCGCCAGA
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SEQ ID NO:23

GL2_209_3_M13F

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CGAGCCCCCGGTACCCCTGAGGCTGGTGGTGCCGGCCACCCAGTGCGGCTCCCTGATTTGGGAAAGGCGGGTGTA
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CGCTCTCCAGTCTCCGCAAGGGAGAGTTCATGACCATTTCCGTACCAGCCCATGCCGGCCAGCTCCCCAGTCACT
GCGCGGGCGGCCAAAGATCGGNGCAGCGACGCTGCGGGCTACCCCAACAATAGACACACCATGACCTGGAGGGGAAC
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SEQ ID NO:24

GL2_209_4_M13R

5 CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
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CTTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCA
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TCTCGCGGATCTCTTTGATCTTACACCCGCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCC
10 TCAGGGTGACCGGGGGCCTGCTGGCCCGGTACTGTTGGTCATGGAGCTGTTGATATCTTCTCCAGACTTGTGCG
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CCTTCGAAGATGTGATCCGCGCGCACATCTCTCGCGGATCTCTTAAACCGAGTCCCNNTTTCATCCAAGAATGNA
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15 GGGTTAAATAAAAAATAAGGGCCGCAAAAAATCGAAGGAATCGAGAAAAACANGCCGCAAAATCGGCACACTAA
TGAACGATAACAATAAGACAGA

SEQ ID NO:25

GL2_131_4_M13F

20 CGCTGCGGGCTCCCGGCCCGGCTCGCCATGGATGGCCGGTGTGACTGAAAGTGGACTAAATGTGANTCTCACCAT
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GGAGAGTGGCGCGCGGATCAACTATCTCGTGAGGGAATTGTCTCNGGAGAGAANCATCACTCTGACCGCCCCACC
AATGANCANCTTTAAGGCTTGCGCATATGATCATCGACAAGCNGGAGGAAGATATCAACAGANTACCATGACCAA
CAGTACCGCGGGACAGACANGCCCCCGNCGACANGAGGCTGGAGGNAGCCGGACCAGC

SEQ ID NO:26

GL2_205_C04_G3F1

25 CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
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CTTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCA
30 CGCCAGCGATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCACTGGACCTGCGCCCCCGTACTC
TCGCGGATCTCTTTGATCTTACACCCGCTTTCCCAATCAGGGAGCCGCACTGGGTGTGCCGGCACCACCAGCCT
CAGGGTGACCGGGGGCCTGCTGGCCGCGGTACTGTTGGTCATGGAGCTGTTGATATCTTCTCCAGCTTGTGCGAT
GATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGACAATTCCCCTC
CGAGATGTTGATCCGCGCGCCACTCTCTCGCGGATCTCTTAAACGATCCCCCTTCTTCCCAATGATGCTTCCA
35 TACTTCTTTTCCGTGCATAAGAAGCCGAAATGGTGAGAGTCACCATTAGGTCCACTTTTCACTCAACACCGGATC
CATGGGCGAGCGGGGCGAGGACGTACCGGGGNGAGATTGGGCTCGAACAGTGGGCAAAGACAGGACAGA

SEQ ID NO:27

GL2_77_4_M13R

40 CGCTGCGGCCTCCCGCCCGCTCCCGCTCGCTCCCGCGGCCCTCGCTCGCCTCGCGCCGGCAGTTTGGGCCTACA
CCTCCCCCTCCCCCGCCAGCCGCCAAAGACTTGACCACGTAACGAGCCCAACTCCCCGAACGCCCGCCCGCGCT
CGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCATTTCGGCTTCTTATGCACGGAAGGA
AGTAGGAAGCATCATTTGGGAAGAAAGGGGAGTCGGTTAAGAGGATCCGCGAGGAGAGTGGCGCGCGGATCAACAT
45 CTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAATGCCATCTTTAAGGCTTTTCGCTA
TGATCATCGACAAGCTGGAGGAAGATATCAACAGCTCCATGACCAACAGTACCGCGGCCAGCAGGCCCCCGGTCA
CCCTGAGGCTGGTGGTNGCCGGCCACCCAGTGCGGCTCCCTGATTGGGAAAGGCGGGTGTAAAGATCAAAGAGATC
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SEQ ID NO:28

GL2_77_5_M13R

50 CGCTGCGGCCTCCCGCCCGCTCCCGCTCGCTCCCGCGGCCCTCGCTCGCCTCGCGCCGGCAGTTTGGGCCTACA
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55 CTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAATGCCATCTTTAAGGCTTTTCGCTAT
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CCTGAGGCTGGTGGTNGCCGGCCACCCAGTGCGGCTCCCTGATTGGGAAAGGCGGGTGTAAAGATCAAAGAGATCCG
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SEQ ID NO:29

GL2_209_4_M13F

CGCTGCGGCCTCCCGCCCGCGCTCGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCAT
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 5 GGAGAGTGGCGCGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAA
 TGCCATCTTTAAGGCTTTTCGCTATGATCATCGACAAGCTGGAGGAAGATATCAACAGCTCCATGACCAACAGTAC
 CGCGGCCAGCAGGCCCCCGGTACCCCTGAGGCTGGTGGTGCCGGCCACCCAGTGC GGCTCCCTGATTGGGAAAGG
 CGGGTGTAAAGATCAAAGAGATCCGCGAGAGTACGGGGGCGCAGGTCCAGGTGGCGGGGGATATGCTGCCAACTCC
 10 ACCGAGCGGGCCATCACCATCGCTGGCGTGCCGCAGTCTGTTTACCAGTGTGTACAGCNAGATTTGCCCTGGT
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 AACCAACAGCCCCCAAATGGGGCCCGGGGCCACAGGCTCCCCCAAGGACANATCNGGAGGCCGGGGGACGGGCC
 CAACGAATCCGGGGAGGCAAGACGAANACATGCAGGGCATAACCCCCCANGGCCACCCCATGAACCTGGGAAGGG
 GACCACCTCTGGGAATGGCNAATCGAGTCAAGCCAGAAAAACCAGCACACG

SEQ ID NO:30

GL2_205_C06_G3F1

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 ACCGATCTTGGCGCCGCGCAGATGACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCCCT
 TGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCACG
 20 CCAGCGATGGTGTATGNGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGGCACCTGGANCTGCGCCCCCGTACT
 CTCGCGGATCTCTTTGATCTTACACCCGCTTTCCCAATCAGTGGAGCCGCACTGGGTGTGCTTGGCACCACCAG
 CCTCAGGGTGACCGGGGTGCTGCTGGCCCGCTACTTGTGTCATGGAGCTGTTGATATCTTCTCCGACAATTC
 TCGATGATCATAGCGAAAGCCTTAAAGATGGCATTTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGACAATTC
 CCTCCGAGATGTTGATCCGCGCGCAATCTCCTCGCGGATCCTCTTAACGAATCCCCTTTCTTCCAAANGATGAT
 25 TCCTANTTCTTTTACCGTGATATAGAAAGCCCCGAAATGGTTGACGAGTCCACATTTAGTCCACACTTTCAGTCA
 CACCCGGGAATCCAATGGGCGAGCGGAGGGACGGAGACGGGGGAAGATGGGCGCCGAACGTTGGGCCAAGAATA
 GAGCAAGAGAGNAGAAGGAAAAANGACAAAGAGCACAAACAGAAAAAGACAAAAAGGNAGCAAGCACACNAAAA
 AA

SEQ ID NO:31

GL2_209_2_M13F

CGCTGCGGCCTCCCGCCCGCGCTCGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCAT
 TCGGCTTCTTATGCACGGAAGGAAGTAGGAAGCATCATTTGGGAAGAAAGGGAGTTCGGTTAAGAGGATCCGCGA
 35 GGAGAGTGGCGCGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAA
 TGCCATCTTTAAGGCTTTTCGCTATGATCATCGACAAGCTGGAGGAAGATATCAACAGCTCCATGACCAACAGTAC
 CGCGGCCAGCAGGCCCCCGGTACCCCTGAGGCTGGTGGTGCCGGACACCCAGTGC GGCTCCCTGATTGGGAAAGG
 CGGGATGTAAGATCAAAG

SEQ ID NO:32

>gi|14141164|ref|NM_006196.2| Homo sapiens poly(rC) binding protein 1
 (PCBP1), mRNA

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 GCCTCGCGCCGGTAGTTTGGGCCTACACCTCCCTCCCCCGCCAGCCGCCAAAGACTTGACCACGTAA
 CGAGCCCAACTCCCCCGAACGCGCCCGCGCTCGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAAT
 45 GTGACTCTCACCATTTCGGCTTCTTATGCACGGAAGGAAGTAGGAAGCATCATTTGGGAAGAAAGGGAGT
 CGGTAAAGAGGATCCGCGAGGAGAGTGGCGCGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAAT
 CATCACTCTGACCGGCCCCACCAATGCCATCTTTAAGGCTTTTCGCTATGATCATCGACAAGCTGGAGGAA
 GATATCAACAGCTCCATGACCAACAGTACCGCGCCAGCAGGCCCCCGGTACCCCTGAGGCTGGTGGTGC
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 50 GCGCAGGTCCAGGTGGCGGGGGATATGCTGCCCCAAGTCCACCGAGCGGGCCATCACCATCGCTGGCGTG
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 55 AGTCTCACTTTGCCATGATGCACGGCGGGACCGGATTCCGCCGAATTGACTCCAGCTCTCCAGAGGTGAA
 AGGCTATTGGGCAAGTTTGGATGCATCTACTCAAACCACCCATGAATCACCATTCCAAATAACTTAATT
 GGCTGCATAATCGGGCGCAAGGCGCAACATTAATGAGATCCGCCAGATGTCCGGGGCCAGATCAAAA
 TTGCCAACCAAGTGGAAAGGCTCCTCTGAGGAGGCTTACTGAGAGGGCATGGGGTGACGCTAGAACAGTGTAGGT
 60 GGCCAGTATCTAATCAATGCCAGGCTTTCTCTGAGAGGGCATGGGGTGACGCTAGAACAGTGTAGGT
 TCCCTCAATAACCCCTTTCTGCTGTTCTCCCATGATCCAACCTGTGTAATTTCTGGTCAGTGATTCCAGGT

TTTAAATAATTTGTAAGTGTTTCAGTTTCTACACAACCTTTATCATCCGCTAAGAATTTAAAAATCACATTCTCTGTTTCAGCTGTTAATGCTGGGATCCATATTTAGTTTATAAGCTTTTCCCTGTTTTTAGTTTTGTTTTGGGTTTTTTGGCTCATGAATTTTATTTCTGTTTGTGCGATAAGAAATGTAAGAGTGGAATGTTAATAAATTTCAGTTTAGTTCTGTAATGTCAAGAATTTAAGAATTAACGATTGGTTAAAAATGCTTCATATTTGAAAAAGCTGGGAATTGCTGTCTT

SEQ ID NO:33

>gi|5453854|ref|NP_006187.1| poly(rC)-binding protein 1; heterogenous nuclear ribonucleoprotein X; alpha-CP1; nucleic acid binding protein sub 2.3; heterogenous nuclear ribonucleoprotein E1 [Homo sapiens]
MDAGVTEGLNVTLTIRLLMHGKEVGSIIIGKKGESVKRIRESGARINISEGNCPERIITLTGPTNAIFKAFAMIIDKLEEDINSSMTNSTAASRPVTLRLVVPATQCGSLIGKGGCKIKEIRESTGAQVQVAGDMLPNSTERAITIAGVPQSVTECVKQICLVMLETLTSQSPQGRVMTIPYQMPASSPVICAGGQDRCSDAVGYPHATHDLEGPPLDAYSIQGOHTISPLDLAKLNQVARQQSHFAMMHGGTGTFAGIDSSSPVKGYWASLDASTQTHELTIPNNLIGCIIIGRQGANINEIROMSGAIKIANPVEGSSGRQVTITGSAASISLAQYLINARLSSEKGMGCS

SEQ ID NO:34

Amino acid transporter (SLC1A5)

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SEQ ID NO:35

>GL3_8.66_A_M13F

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SEQ ID NO:36

>GL3_8.66_A_M13R Direction: anti-sense

CTCCTAGGGCCAAGGAACCCGGGCGCTCCGAACCTCCAGCTTTCGGACATCTGGCACACGGGGCAGAGCAGAGAAAGCTCAGCGCCAGCCTGGGGAATTTAAACACTCCAGCTTCCAAGAGCCAAGGAACCTCAGTGCTGTGAACTCACAACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCTTAGGAACGTCGGGTCTTGGAAGGAGCCCAAGCGCTCCAGCCAGCTTCCAGGCGCTAAGAAACCCGGTGCTTCCCATCATGGTGGCCGATCTCCTCGAGACTCCAAGGGGCTCGCAGCGCGGAGCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGGACCAAGGCGCGGCAGCAGGCGGCTACTGCGGTTCCCGGGACCAGGTGCGCCGCTGCCTTCGAGCCAACCTGCTTGCTGCTGACAGTGCTGGCCGTGGTGGCCGCGTGGCGCTGGGACTGGGGGTGTCGGGGGCGGGGGGTGCGCTGGCGTGGTGGGCTGGAGCGCTTGAGCGCCTTCGTCTTCCCGGCGAGCCGAACCCAGCACACTGGAGCCACC

SEQ ID NO:37

>GL3_8.66_B_M13F Direction: sense

CTATAGGGCGAATGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGATGGATATCTGCAGAATTCGCCCTTCTCTCGGCATGGACGAGCTGTACAAGGAGGAGGCCGCCAAGGCCGGTGGCAGCGGTGGCTCCAGTGCTGGGTTCGGGCTCGCCCGGAAGACGAAGGCGCTCAAGCGCTCCAGGCCCAACGCCAGCGCACCCCCGGTCCCCGACACCCAGTCCCAGCGCCACGCCGGCCACCACGGCCACCACTGTCAGCAGCACAAAGCAGGTTGGCTCGAAGGCAGCGGCGCACCTGGTCCCAGGAACCGCAGTAGCCGCTGCTGCCGCGCCTTGGTCTCGATGGAGGCCAGCGCCAGGCCCCGTGGCGGTGGGCTCCGCCGCTGCGAGCCCCCTTGGAGTCTCGAGGAGGATCGGTCAACCATGATGGGAAGCACCGGGGTTTCTTAGCGCCTGGAAGCTGGCTGGGAGCGCTTGGGCTCCTTCCCAGGACCCGACGTTCTTAGGACTGAGTTGAGTAACAGCACCTGGAGACTGGAACCTTGGAGGGCTCCTTAGAGTTGCGAGTTCACAGCACTGAAGTTCCTT

GGCTCTTGGAAGCTGGAGTGTTTAAATTCCCCAGGCTGGGCGCTGAGGCTTCTCTGCTCTGCCCCGTGTGCCAGA
TGTCCGAAAGCTGGGAGTTCGGAGCGCCCGGGTTCTTGGCCCTAGGAG

SEQ ID NO:38

>GL3_8.66_B_M13R Direction: anti-sense

CTCCTAGGGCCAAGGAACCCGGGCGCTCCGAACCTCCAGCTTTTCGGACATCTGGCACACGGGGCAGAGCAGAGAA
GCCTCAGCGCCCAGCCTGGGGAATTTAAACACTCCAGCTTCCAAGAGCCAAGGAACCTTCAGTGCTGTGAACTCGC
AACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCTTAGGAACGTTCGGGTCTTG
GGAAGGAGCCCAAGCGCTCCCAGCCAGCTTCCAGGCGCTAAGAAACCCCGGTGCTTCCCATCATGGTGACCGATC
CTCCTCGAGACTCCAAGGGGCTCGCAGCGGCGGAGCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGG
ACCAAGGCGCGGCAGCAGGCGGCTACTGCGGTTCCCGGGACAGGTGCGCCGCTGCCTTCGAGCCAACCTGCTTG
TGCTGCTGACAGTGGTGGCCGTGGTGGCCGGCGTGGCGCTGGGACTGGGGGTGTCGGGGACCGGGGGTGCCTGG
CGTTGGGCCCTGGAGCGCTTGAGCGCCTTCGTCTTCCCGGGCGAGCCGGAACCCAGCACACTGGAGCCACCGCTGC
CACCGGCCTTGGCGGCCTCCTCCTTGTAACAGCTCGTCCATGCCGAGAGAAGGGCGAATTCTGCAGATATCCATCA
CACTGG

SEQ ID NO:39

>GL3_8.66_C_M13F Direction: anti-sense

CTCCTAGGGCCAAGGAACCCGGGCGCTCCGAACCTCCAGCTTTTCGGACATCTGGCACACGGGGCAGAGCAGAGAA
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AACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCTTAGGAACGTTCGGGTCTTG
GGAAGGAGCCCAAGCGCTCCCAGCCAGCTTCCAGGCGCTAAGAAACCCCGGTGCTTCCCATCATGGTGGCCGATC
CTCCTCGAGACTCCAAGGGGCTCGCAGCGGCGGAGCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGG
ACCAAGGCGCGGCAGCAGGCGGCTACTGCGGTTCCCGGGACAGGTGCGCCGCTGCCTTCGAGCCAACCTGCTTG
TGCTGCTGACAGTGGTGGCCGTGGTGGCCGGCGTGGCGCTGGGACTGGGGGTGTCGGGGGCGGGGGTGCCTGG
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CACCGGCCTTGGCG

SEQ ID NO:40

>GL3_8.66_C_M13R Direction: sense

GATCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTCTCTCGGCATGGACGAGCTGTACAAGGAGGAGGC
CGCCAAGGCCGGTGGCAGCGGTGGCTCCAGTGTGCTGGGTTCGGCTCGCCCGGGAAGACGAAGGCGCTCAAGCG
CTCCAGGCCCAACGCCAGCGCACCCCCGGCCCCGACACCCCCAGTCCCAGCGCCACGCCGGCCACCACGGCCAC
CACTGTGCAGCACAAGCAGGTTGGCTCGAAGGCAGCGGCGACCTGGTCCCGGGAACCGCAGTAGCCGCTGC
TGCCGCGCCTTGGTCTCGATGGAGGCCAGCGCCAGGCCCGCTTGGCGGTGGGCTCCGCCGCTGCGAGCCCCCTT
GGAGTCTCGAGGAGGATCGGCCACCATGATGGGAAGCACCGGGGTTTCTTAGCGCTTGAAGCTGGCTGGGAGCG
CTTGGGCTCCTTCCAGGACCCGACGTTCTTAGGACTGAGTTGAGTAACAGCACCTGGAGACTGGAACCTTTGGAG
GGCTCCTTAGAGTTGTGAGTTACAGCACTGAAGTTCTTGGCTCTTGAAGCTGGAGTGTTTAAATTCCCCAGG
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CTTGGCCCTAGGAG

SEQ ID NO:41

>GL3_8.66_D_M13F Direction: N/A

ACTATAGGGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCGC
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GTTCCGGCTCGCCCGGGAAGACGAAGGCGCTCAAGCGCTCCAGGCCCAACGCCAGCGCACCCCCGGCCCCGACA
CCCCAGTCCCAGCGCCACGCCGGCCACCACGGCCACCACTGTCAGCAGCACAAAGCAGGTTGGCTCGAAGGCAGC
GGCGCACCTGGTCCCGGGAACCGCAGTAGCCGCTGCTGCCGCGCTTGGTCTCGATGGAGGCCAGCGCCAGGC
CCCCGTTGGCGGTGGGCTCCGCCGCTGCGAGCCCCCTTGGAGTCTCGAGGAGGATCGGCCACCATGATGGGAAGCA
CCGGGGTTTCTTAGCGCCTGGAAGCTGGCTGGGAGCGCTTGGGCTCCTTCCAGGACCCGACGTTCTTAGGACTG
AGTTGAGTAACAGCACCTGGAGACTGGAACCTTTGGAGGGCTCCTTAGAGTTGTGAGTTACAGCACTGAAGTTCC
TTGGCTCTTGAAGCTGGAGTGTTTAAATTCCCCAGGCTGGGCGCTGAGGCTTCTCTGCTCTGCCCCGTGTGCCA
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SEQ ID NO:42

>GL3_8.66_D_M13R Direction: anti-sense

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GCCTCAGCGCCCAGCCTGGGGAATTTAAACACTCCAGCTTCCAAGAGCCAAGGAACCTTCAGTGCTGTGAACTCAC
AACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCTTAGGAACGTTCGGGTCTTG
GGAAGGAGCCCAAGCGCTCCCAGCCAGCTTCCAGGCGCTAAGAAACCCCGGTGCTTCCCATCATGGTGGCCGATC

CTCCTCGAGACTCCAAGGGGCTCGCAGCGGCGGAGCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGG
ACCAAGGCGCGGCAGCAGCGGCTACTGCGGTTCCCGGGACCAGGTGCGCGCTGCTTCGAGCCAACCTGCTTG
TGCTGCTGACAGTGGTGGCCGTGGTGGCCGCGCTGGCGCTGGGACTGGGGGTGTCGGGGGCGGGGGTGCCTGG
CGTTGGGCCTGGAGCGCTTGAGCGCTTCGTCTTCCCGGGCGAGCCGGAACCCAGCACACTGGAGCCACCGCTGC
5 CACCGGCCTTGGCGGCCTCCTCCTTGTACAGCTCGTCCATGCCGAGAGAAGGGCGAATTCTGCAGATATNCATCA
CACTGGCGG

SEQ ID NO:43

>gi|5032092|ref|NM_005628.1| Homo sapiens solute carrier family 1 (neutral
10 amino acid transporter), member 5 (SLC1A5), mRNA
GTAACCGCTACTCCCGGACACCAGACCACCGCCTTCCGTACACAGGGGCCCCGCATCCACCCCTCCCGGAC
CTAAGAGCCTGGGTCCCCTGTTTCCGGAGGTCCGCTTCCCGGCCCCAGATTCTGGCATCCAGCCCTCA
GTGTCCAAGACCCAGGCAGCCCGGGTCCCCGCTCCCGGATCCAGGCGTCCGGGATCTGCGCCACCAGAA
15 CCTAGCCTCCTGCAGACCTCCGCCATCTGGGGGCACCTCAACCTCCTGGAGCCAAGGGCCCCCAGCTCCAC
CCAGAGAACTCTCGTATTCCAGCTCCTAGGGCCAAGGAACCCGGGCGCTCCGAACCTCCAGCTTTCGG
ACATCTGGCACACGGGGCAGAGCAGAGAAGCTCAGCGCCAGCCTGGGGAATTTAAACACTCCAGCTTCC
AAGAGCCAAGGAACCTCAGTGCTGTGAACCTCACAACCTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGT
GCTGTTACTCAACTCAGTCTTAGGAACGTCGGGTCTGGGAAGGAGCCCAAGCGCTCCAGCCAGCTTCC
AGGCGCTAAGAAACCCCGGTGCTTCCCATCATGGTGGCCGATCCTCCTCGAGACTCCAAGGGGCTCGCAG
20 CGGCGGAGCCCCACGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGGACCAAGGCGCGGCAGCAGGCGG
CTACTGCGGTTCCCGGACAGGTGCGCCGCTGCCCTTCGAGCCAACCTGCTTGTGCTGCTGACAGTGGTG
GCCGTGGTGGCCGCGTGGCGCTGGGACTGGGGGTGTGGGGGCGGGGGTGGCGCTGGCGTTGGGCCCGG
AGCGCTTGAGCGCCTTCGTCTTCCCGGGCGAGCTGCTGCTGCGTCTGCTGCGGATGATCATCTTGCCGCT
GGTGGTGTGACGCTTGATCGGCGGCGCCGCGCAGCCTGGACCCCGGCGCGCTCGGCCGTCTGGGCGCCTGG
25 GCGCTGCTCTTTTCTGGTCAACACGCTGCTGGCGTGGCGCTCGGAGTGGGCTTGGCGCTGGCTCTGC
AGCCGGGCGCCGCTCCGCCGCCATCAACGCCTCCGTGGGAGCCGCGGGCAGTGCCGAAAATGCCCCCAG
CAAGGAGGTGCTCGATTCTGCTTCTGGATCTTGCGAGAAATATCTTCCCTTCCAACCTGGTGTCAGCAGCC
TTTCGCTCACTACTCTACCACCTATGAAGAGAGGAATATCACCGGAACCAGGGTGAAGGTGCCCCGTGGGGC
AGGAGGTGAGGGGATGAACATCCTGGGCTTGGTAGTGTCTTGGCATCGTCTTGGTGTGGCGCTGCGGAA
30 GCTGGGGCCTGAAGGGGAGCTGCTTATCCGCTTCTTCACTCCTTCAATGAGGCCACCATGGTCTTGCTC
TCCTGGATCATGTGGTACGCCCCCTGTGGGCATCATGTTCTGCTGGTGGCTGGCAAGATCGTGGAGATGGAGG
ATGTGGGTTTACTCTTTGCCCGCCTTGGCAAGTACATTCTGTGCTGCCTGCTGGGTACGCCATCCATGG
GCTCCTGGTACTGCCCCCTCATCTACTTCTTACCCGCAAAAACCCCTACCGCTTCTGTGGGGCATC
GTGACGCGCGCTGGCCACTGCCTTTGGGACCTCTTCCAGTTCCGCCACGCTGCCGCTGATGATGAAGTGCG
35 TGGAGGAGAATAATGGCGTGGCCAAGCACATCAGCCGTTTTCATCCTGCCCATCGGCGCCACCGTCAACAT
GGACGGTGCCGCGCTCTTCCAGTGCGTGGCCGCAAGTGTTCATTGCACAGCTCAGCCAGCAGTCTTGGAC
TTCGTAAAGATCATCACCATCCTGGTCAAGGCCACAGCGTCCAGCGTGGGGGAGCGGGCATCCCTGCTG
GAGGTGCTCCTCACTTGGCCATCATCCTCGAAGCAGTCAACCTCCCGGTGACCATATCTCCTTGATCCT
GGCTGTGGAGTGGCTAGTCGACCGGCTCCTGTACCGTCTCTCAATGTAGTAAGGTGACGCTCTGGGGGAGGA
40 CTCCTCCAAAATTATGTGGACCGTACGGAGTCGAGAAGCACAGAGCCTGAGTTGATAACAAGTGAAGAGTG
AGCTGCCCCCTGGATCCGCTGCCAGTCCCCACTGAGGAAGGAACCCCTCCTCAAAACACTATCGGGGGCC
CGCAGGGGATGCCACGGTGCCTCTGAGAAGGAATCAGTCATGTAAACCCCGGAGGGACCTTCCCTGCC
CTGCTGGGGGTGCTCTTTGGACACTGGATTATGAGGAATGGATAAATGGATGAGCTAGGGCTCTGGGGGT
CTGCCTGCACACTCTGGGGAGCCAGGGGCCCCAGCACCCTCCAGGACAGGAGATCTGGGATGCCTGGCTG
45 CTGGAGTACATGTGTTCAAGGGTTACTCCTCAAAACCCCGAGTTCTCACTCATGTCCCCAATCAAGG
CTAGAAAACAGCAAGATGGAGAAATAATGTTCTGCTGCGTCCCCACCGTGACCTGCCTGGCCTCCCCGTG
CTCAGGGAGCAGGTACAGGTACCATGGGGAATTCTAGCCCCACTGGGGGGATGTTACAACACCATGC
TGTTTATTTTGGCGCTGTAGTTGTGGGGGATGTGTGTGTCACGTGTGTGTGTGTGTGTGTGTGTGTGTGT
50 TGT
CACAATAACAGAAACTCCAGGGACTCTGGGGAGAGGCTGAGGACAAATACCTGCTGTCTACTCCAGAG
GACATTTTTTTTAGCAATAAAATTGAGTGTCAACTATTTAAAAA

SEQ ID NO:44

>gi|5032093|ref|NP_005619.1| solute carrier family 1 (neutral amino acid
55 transporter), member 5; baboon M7 virus receptor; RD114 virus receptor;
neutral amino acid transporter B [Homo sapiens]
MVADPPRDSKGLAAAEPTANGGLALASIEDQGAAGGYCGSRDQVRRCLRANLLVLLTVVAVVAGVALGL
GVSGAGGALALGPERLSAFVFPGEILLRLLRMIILPLVVCSLIGGAASLDPGALGRLGAWALLFFLVTTL
LASALGVGLALALQPGAASAINASVGAAGSAENAPSKEVLDSFLDLARNIFPSNLVSAAFRSYSTTYEE
60 RNITGTRVKVPVGQEVGMNILGLVFAIVFGVALRKLGPGEILLIRFFNSFNEATMVLVSWIMWYAPVG
IMFLVAGKIVEMEDVGLLFARLGKYILCCLLGHAIHGLLVLP LIYFLFTRKNPYRFLWGI VTPATAFGT

SSSSATLPLMMKCVEENNGVAKHISRFILPIGATVNMDDGAALFQCVAAVFIAQLSQSLDFVKIITILVT
ATASSVGAAGIPAGGVLTLAILLEAVNLPVDHISLILAVDVLVDRSCTVLNVEGDALGAGLLQNYVDRTE
SRSTEPELIQVKSELPLDPLPVPTEEGNPLLKHRYGPAGDATVASEKESVM

5 SEQ ID NO:45

Chromobox homologue 6

>GL3_37C_2_M13F

ACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
CGCCCCGGCCCCCTTGCCCGGGCCCCCGCCGAGCGCCCTTTGTGATCACCCTTCAGGTCAGGATGATGCGGTCCG
10 CTGGGTCATCCCGCGNCTTACACCTTGCGGTTGATGATGCGCACCGTCTCCGAGAAAGGGCGAAATGAGGCGGGCA
GCAGTCCGGGGCTGCCCCCTGCAGGTCGCGGGCGGGGACGGGCGGGACATACGGTTGGGCAAGNCGGG
CCGGCGAATGTTCTTATACTTGAAGCCCGGTTGCCACGGGATTAGACGCCTTTGGGAGATTGCACGCATATGG
GGCAAAGGAAGGGCNACCTTGCCCGCTCGGGCNTTTNGACACGGAAGGNAATTTGCCACATTCACCTTGAATT
15 TGCGCCAGAATANGGGCNCCTTNCGTGAGCGACCACTTTGGGCCCCCAGGGGANGNACGCCGTTTATCA
TCAAAGAGGGAAAAGGCNAAAAAAGCGTTNTATCAGTAGAGGGGACAGGGGAATTATTAGGGGGGATTAC
CCCCCCCAGTTACAATTTTACCATATTTGAGGAGGAGNCCGCCANAGTATTAAACATAGGACGTGTNCAAACG
GGGACNTTACACCAGCATTANCAATTTCCGCAATTTATTATAGTATGGGGATTNCAGAACAAANGTGGGCCCTTT
TGTCGAAAAATTTAGGAATAGGTCCCCACGG

20 SEQ ID NO:46

>GL3_35L_1_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCGAGGAGAATCCTGGACTCGCGGCTCATTGCAGCCTTCGAACAAAAGGAGAGGGGAGC
GTGAGCTGTATGGGCCCAAGAAGAGGGGACCCAAACCCAAACTTTCTCTGAAGGCGCGGGCCAGGCCGAGG
25 CCCTNTCCGCATCAGTGATGTGCATTTCTCTGTCAAGCCGAGCGCCAGTGCCCTCCTCGCCCAAGCTGCACTCCAG
CGCAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCCGCCGTCCCCTGCCCGCCCGGA
CCCGCAGGGGGGAGCCCCGGACTGCGCCCGCCATTTGCGCCTTCTCGGAGACGGTGCGCATCATCAACCGCCA
AGGTGAAGCCGCGGGAGCCCAAGGCGGAACCGCATCATCCTGAACCTGAAGGTGATCGGAACAAGGGCGCTGGCA
CGGCAGGGGGGCGCCGGGCAAGGGGGCGGGGACGCTGGCCCGCCCAAAAAAGGNTCNCCTATCNGCGGGGAAAC
30 CCGGCGGTGTAATAGGGGCAAAGAGGCAAGAACAGGTACCAGGCAAAGGAAGCCGGGTACATGGCAGGTNCGCG
GNCANAGAAACCCAGCAACACTTGGGAGGCCACACCGGGTNGCNAACCGGACCTTTNGGGGGGGCCTCACATC
ACCNATGGTACCAAGGTCGTACCAATCGAGCACGGACAAGAAAGGGGGCGAAATTC

SEQ ID NO:47

>GL3_35L_3_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCGAGGAGAATCCTGGACTCGCGGCTCATTGCAGCCTTCGAACAAAAGGAGAGGGGAGC
GTGAGCTGTATGGGCCCAAGAAGAGGGGACCCAAACCCAAACTTTCTCTGAAGGCGTGGGGCCAGGCCGAGG
35 CCCTCCGCATCAGTGATGTGCATTTCTCTGTCAAGCCGAGCGCCAGTGCCCTCCTCGCCCAAGCTGCACTCCAGCG
CAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCCGCCGTCCCCTGCCCGCCCGGACC
CGCAGGGGGGCAAGCCCCGGAAGTNGCCCGCCCAATTTGCGCCTTCTCGGAGACCGGTGCGCATCATCAACCGC
40 AAGTGAAGCCGCGGGAGCCAAGCGGAACCGATCATCCTGAAACCTGAAGGTGATCGGACAAGGGCGCTGGCGGAC
GGGGCGCGCGGGCAGGGGGGCGGGGGCGCCTGGGCCCCGGCCCCCAANAGTCCCCCACCATCAGGGCGAGG
GAAACCCCGGGGAGAAAGTAGCGGGCAAAANGAAGCCAANAGGAAANGTTCAACAAGGAGAGAAGAACNGA
CGACCANGGCGAGATCCCGGGGAAGAGAAACGCNCAAGGCAAAACAAGATTGGGAGAAGCNACAACNGGTGAGC
ACAACAGCCGGGGCCACTAGGCGGCGGGNACCTACCCTCCCCTATTGGAACGCAGCNCGGGCANCAATTGCCGA
45 GAAAGAAAGGGGGGCGAATTCTNCGA

SEQ ID NO:48

>GL3_35L_4_M13F Direction: N/A

ACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
CGCCCCGGCCCCCTTGCCCGGGCGCCCCCGCCGGCCAGCGCCCTTGTCGATCACCCTTCAGGTTTCAGGATGATGCG
50 GTTCCGGCTTTGGGTCATCCCGGGGGCTTACCTTTGCGGGGTTGACTGATGCGCACCGGACATCTGAGAAAGGG
CGAAATGGGACGGGACGAGATCCGGGGCNTGCCCCCCTTGCCGGGGGGACTTCCAGGGGACGGGGGANGA
CAAGGGGGGAACGGGGACGGGTGAACCAATTACCGNGGTGGGCCAGCCGGGCGGGGAATGGGTCCCTTCTTGGA
AGACCGGGTGCCAA

55

SEQ ID NO:49

>GL3_37C_1_M13F Direction: sense

ACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
CGCCCGGGCCCCCTTGCCCTGGAGCCCCCGCCGAGCAGGCCATTGTGAGAATTCAACTTTCAAGGNTNCAAG
60 GGATGAATTGCGNGGTCCCGGCTNTATGGGGATTCCNCAGAAGGGACTTTTCAACCTTTTGCCAGGGATATGGAA

CGTGGNATTTGCCGGCCAAACCCCGGGGTNACTCCCCAGAAAGGAAAAAGGGGGGCGGGAAAAAATTTGGGCGCT
GGGGGCCGACGGC

SEQ ID NO:50

>GL3_35L_1_M13F Direction: N/A

ACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCA
GCGCCCGGGCCCCCTTGCCCCGGGCCCCCGCCCGCCNAGCGGCCCTTTGTGCGATCAACCTTCAGGTCAGGATGA
TGGGTTCCGCTTTGGGCTTCCCGGCGGGTTTCACTTGCGGGTTGATGATGCGGCAACCCGGGTCTTCCCAGA
AGAACAGGGGGCGGACAATTGGNGCGCAGGGGC

SEQ ID NO:51

>GL3_35L_3_M13F Direction: N/A

ACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
CGCCCCGGGCCCCCTTGCCCCGGGCCCCCGCCCGCCAGCGCCCTTGTCGATCACCTTCAGGTNCAGGATGATGCGGTT
CCGCTTGGGCTCCCGCGGCTTCACTTGCGGTTGATGATGCGCACCGTCTCCGAGAAGGGCGAAATGGGCGGGCG
CAGTCCGGGGCTGCCCCCTTGCGGGATCCGGGCGGGGACCGGCGGGCACCATACGGGTGGCAGCGGCG
GGAATGTCCTTCTTGAAGCCGGTGACGCTTGCGCTTGAAGTTGCAGCTTGGGCCAAGG

SEQ ID NO:52

>GL3_35L_4_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCGAGGAGAACATCCTGGACTCGCGGCTCATTCGAGCCTTCGAACAAAAGGAGAGGGAGC
GTGAGCTGTATGGGCCCCAAGAAGAGGGGACCCAAACCCAAAACCTTTCTCCTGAAGGCGCGGGCCAGGCCGAGG
CCCTCCGCATCAGTGATGTGCAATTTCTGTCAAGCCGAGCGCCAGTGCTCCTCGCCCAAGCTGCACTCCAGCG
CAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCCGCCGTCCCCTGCCCCGCCCCGGACC
CGCAGGGGGGCGAGCCCCGACTGCGCCCCGCCCATTTGCGCCTTCTCAGAGACGGTGCGCATCATC

SEQ ID NO:53

>GL3_35L_PCR_G3F1 Direction: N/A

GACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCC
AGCGCCCCGGCCCCCTTGCCCCGGGCCCCCGCGCGGCCCTTTATACCTTCAGTTTCAGATGATGCGGTTCCGCTTGGG
CTCCCGCGGCTTCACTTGCGGTTGATGATGCGCACCGTCTCCGAGAAGGGCGAAATGGGCGGGCGCAGTCCGGG
GCTGCCCCCTTGCGGTTCCGGGCGGGGACGGGCGGGACATACGGTGGCAGCGGCGGATGTCTTCTTCTGAG
CCGGTGACGGCTGCGCTGGAGTGACGCTTGGGCGAGGAGGCACTGGCGCTCGGCTTGACAGAGAAATGCACATC
ACTGATGCGGAGGGCTCGGCCCTGGGCCCCGCGCCTTCAGGAGGAAAGTTTGGGTTTGGGTCCCCTCTTCTTGGG
CCATACAGCTCAGCTCCCTCTCCTTTGTTTGAAGGCTGCAATGAGCCGCGAGTCCAGGATGTTCTCCTCGGG
CTCCCAAGTGCTGT

SEQ ID NO:54

>GL3_37C_1_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCGAGGAGAACATCCTGGACTCGCGGCTCATTCGAGCCTTCGAACAAAAGGAGAGGGAGC
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CCCTCCGCATCAGTGATGTGCAATTTCTGTCAAGCCGAGCGCCAGTGCTCCTCGCCCAAGCTGCACTCCAGCG
CAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCCGCCGTCCCCTGCCCCGCCCCGGACC
CGCAGGGGGGCGAGCCCCGACTGCGCCCCGCCCATTTGCGCCTTCTCGGAGACGGTGCGCATCATCAACCGCAAGG
TGAAGCCGCGGGAGCCCAAGCGGAACCGCATCATCTGAACCTGAAGGTGATCGACAAGGGCGCTGGCGGCGGGA
GGCGCCGGGCGAGGGGGCCGGGNCGCTGGCCCCGCCCAAGTCCCCTCGCGGAAACCCGCGGTAAATAGGCAAAG
AAGCAAGGAAGGTGAGGCGAGAGGCGGTCCCTGCGTCCGNAGAAACCCAGCACACCTGGACGGCCACCGATGCCA
CNGGCCTGGGGGACTCCTCCTGGTACAGGTGCGCACATGCCGG

SEQ ID NO:55

>GL3_37C_2_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCGAGGAGAACATCCTGGACTCGCGGCTCATTCGAGCCTTCGAACAAAAGGAGAGGGAGC
GTGAGCTGTATGGGCCCCAAGAAGAGGGGACCCAAACCCAAAACCTTTCTCCTGAAGGCGCGGGCCAGGCCGAGG
CCCTCCGCATCAGTGATGTGCAATTTCTGTCAAGCCGAGCGCCAGTGCTCCTCGCCCAAGCTGCACTCCAGCG
CAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCCGCCGTCCCCTGCCCCGCCCCGGACC
CGCAGGGGGGCGAGCCCCGACTGCGCCCCGCCCATTTGCGCCTTCTCGGAGACGGTGCGCATCATCAACCGCAA
GGTGAAGCCGCGGGAGCCCAAGCGGAANCGCATCATCCATGAACCTGAA

SEQ ID NO:56

>GL3_37C_PCR_G3F1 Direction: N/A

ACGCAGGACGCTCTCGCTGAACCTCTTGCTCTTGCCCTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
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CGCTTGGGCTCCCGCGGCTTCACCTTGCGGTTGATGATGCGCACCGTCTCCGAGAAGGGCGAAATGGGCGGGCGC
AGTCCGGGGCTGCCCCCTGCGGGTCCGGGCGGGGACGGGACGGCGGGACATACGGTGGCAGCGGCGGATGTCC
TTCTTGAGCCGGTGACGGCTGCGCTGGAGTGCAGCTTGGGCGAGGAGGCACTGGCGCTCGGCTTGACAGAGAAA
TGCACATCACTGATGCGGAGGGCTCGGCTGGGCCCCGCGCCTTCAGGAGGAAAGTTTGGGTTTGGGTCCCCCTC
TTCTTGGGCCCCATACAGCTCACGCTCCCTCTCTTTTGTTCGAAGGCTGCAATGAG

SEQ ID NO:57

>gi|10140848|ref|NM_014292.1| Homo sapiens chromobox homolog 6 (CBX6), mRNA

ATTATGGGCTGTGGGTGCCGCTGAGCAAGATGGAGCTGTCTGCAGTGGGCGAGCGGGTCTTCGCGGCCGA
ATCCATCATCAAACGGCGGATCCGAAAGGGACGCATCGAGTACCTGGTGAAATGGAAGGGGTGGGCGATC
AAGTACAGCACTTGGGAGCCCGAGGAGAACATCTGGACTCGCGGCTCATTTGCAGCCTTCGAACAAAAGG
AGAGGGAGCGTGAGCTGTATGGGCCCAAGAAGAGGGGACCCAAACCAAACTTTCTCTGAAGGCGCG
GGCCAGGCCCGAGGCCCTCCGCATCAGTGATGTGCATTTCTGTCAAGCCGAGCGCCAGTGCCTCTCTCG
CCCAAGCTGCACTCCAGCGCAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCC
GCCGTCCCCCTGCCCCGCCCCGACCCGAGGGGGGACGCCCGGACTGCGCCCCGCCATTTTCGCCCTTCTC
GGAGACGGTGCGCATCATCAACCGCAAGGTGAAGCCGCGGGAGCCCAAGCGGAACCGCATCATCTGAAC
CTGAAGGTGATCGACAAGGGCGCTGGCGGCGGGGGCGCCGGGAGGGGGCGGGGCGCTGGCCCCGCCCA
AAGTCCCCCTCGCGGAACCGCGTTATAGGCAAGAGCAAGAAGTTTCAGCGAGAGCGTCTGCGTACACAGAT
CCGCCACATGAAGTTTCGGCGCCTTTGCGCTGTACAAGCCTCCGCCCGCCCCCTGGTAGCCCCCTCCCC
GGCAAGGCTGAGGCCTCAGCCCCGGGCCCTGGGCTACTTCTGGCCGCCCGCCCGCCCCCTACGACGCCC
GCAGCTCTGGCTCCTCCGGCTGCCCTCGCCTACACCACAGTCTCTGACCCCGACGACACGCCCCCAA
GCTCCTCCCCGAGACCGTGAGCCCATCCGCCCCAGCTGGCGCGAGCCGAGGTGCTCGACCTGTCCCTC
CCTCCCGAGTCCGCAGCCACCAGCAAGCGGGCACCGCCTGAGGTCAAGCTGCTGCCGCCCGCCGACCTC
CCACGGCCCCCTGAGCCCGCCGGTGCCCTCTCCGAGCCCGAGGCTGGGGACTGGCGCCCCGAGATGTCACC
CTGCTCCAATGTGGTCTGTACCGATGTACCAGCAACCTCTGACGGTCACAATCAAGGAATTCTGCAAC
CCTGAGGATTTTCGAGAAGGTGGCTGTGGGTTAGCAGGCGCCGCTGGGGGCGGTGGCAGCATTGGGGCGA
GCAAGTGAGGGGGCTCCACCAAGGAGGGGGGCTTGGGGGGGCGCTCCTGCCCGAAGTCATACTCTTGCTC
CCACCCACCCCTTGCCCCCAGCCCTCTCTCCCTGTGCTTTGCTTGTCTCAAATGGCTCGGTGTTGACCCA
GGGATGGGGCTGGGTAGTTGGGGTCCAGAAAGCCGGGGTAGGGGCCACCTGGAATGGGGCAGGGGAA
GGGCACACCCCTGCCCCATGCATGGTAGCCATGAGCCATGGGTGGTTTCTGGAAGCCCTAGAACTAGGGTTCC
TCTGCCCCCTTCCACATCCCACCTGTCTCTCTAGCTTGTCTTCTGCTCTCTGCTGCGGCGCTGATTTCTC
GGTGCTAACCTGGCAGCTGTGGGGCCCTTAGGAGCCCCCACCGAGGGTGGACACAGTCCCTTTCTCTTCC
TGCAGATGCCCTAGGCAGGAGGAGGGCTTCTGCTGTGTTGGCAAAGTCCAGGCAGAGGCCAAGGATGAG
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AACGGTGGGAGGAACTGGCAGAGGGTGCAGCTGGCCACAGCCTCCCGCATCTAAAGGCCCTTCAGTTC
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GTCCGTGGGTTTCATACATGCATTGGGTGCTAGGCCCCAGGCTGCCGGGTGGCACCCCTTTACAGTTCTTT
GAACAGGGGCATTGAAGGCCCTGGACTGCCCTCAGTGGCTGAGGCTGGGGACAGGCTTGGGTCTGGAG
GTTTGTCTGTGAAGTCACCAGGCCCTCCCTCTGGCCAGGTGTGCTGGGGGACCGTGCCCCCACCCCT
CCTGCCCTCTCAGGGTGGTACAGCCCAACCTGTGCGACCTTCACTTACATCATGGTGGGGACCGAGATA
GAGAGGGAGACCCCATTCGAAGCTCCCTCTTCTCCGGGTGTTTGGGGAGGATGCTGAAGAATCCATTCC
CGAGGGCCTCCCGGCTTGTCCAGCCCTCTTTTGTCTTGTGACACGGAGGCTTTCTCACAGCCAGCCT
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CCCGTGCCAGTGGCAGAGGCCACAGCCCCAGCCTTAGGCCAGGCCCTGGGAGGGCAGGCAGGCAAGGGG
AGACCAGAGGGTCTGTGTTCTCCAGGAGATGAGGGTGTGGTCCAGAAATGGGACCGGGGCCCCGCTG
GCCAGCCCTGGGCCACTTCCCGGGTCTCCATTGTGCGTGGGTGGCGTGTTCAGGCGTGGCTGGAGCTGG
CTTCTGGCTGTGCTGCCATGGGCCCCCTCCCTCAGAAGCAGTTGGCAGGAGCCGATCAGAACCCTAGC
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CTTTTTTGTAAAGAAGTTGTGTTTTTTCAGAGGTGATTTTATGACAGGAAAGTGAAAGAATTAGTTTTGCAA
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CAGGATGGGGCGGAGGCGCTGGGCCCAGCTGGCAGGTCCCCTGGCATCGCAGGCACTGTGGAGAGGGCCTG
GACCCAGATCTCCACACCCGTGCTTGCTCAAAGGGAAGGACAACAGCGGGCCCCGGGAGCTAACCCAAG
CTGCAGGTCCCGGCAAGCTGAGGTTTGGGAGGGTGGGGTGTGCTACTGGTGATTTTCTCCAGGGGGCTGG
TGAGTGGGCAGTTTGGTTTCTTGCCCCCTTCTGTTCCCTTCCAGTTGTTGGGCCATCTGGTCCCCACCA
5 CCGCCACCCTATGGGGGAGACCTCCCTCCCCACGGGTACCCCTAAAGCCCAACCTCTCTGAGCCTCCC
TGGCCTGAAAGGGGATGCAGGCTTCAGGAGGCAAGAAGCTGGGCCCCCTGGGGGTGGCTGGGGAGAGGGAA
TGCAATTTCCCTTGCCACAGGTGGTCTGCTTCTGCTGGCCTGAGCTCCAAGTGGAGCAGCCCCGGGCCAGCC
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10 GACCGAGGGTGAGTGGAGCCTCCTTCCCTCCCTCTCTAGTACCCCCGCCTCCACACACTTGCACGGATC
GGCCTCCCTTGGGAGATCAGCCTCCATGGGCCCCCTCGTCCACCCTTGCTGCTTTCCATTTGCCTAATTAC
CAAGCAGAAGTTGCAATCTGGTTTGCTTTATTTTGTATGTGAAATAACCCCCAAAGCCCAATCTCCTCC
TACGTTCAATATTGGTTGGGGCATCCGTCATCTCCCTTAAGTGCGCCCCCTCCCCACCCAAGTATCAT
GGAACCGGTGAGGTCTGGTGTCTCTGGTTTGAGACGGTAAGTTGGGACCCATCCCTGTCTGGGTGCCCA
CTCTGACCTTTAGTTTGCCCTTCTGTGAAATGGGTGTATTGGGTAGCAAGCCCTCTTCAGAAAGCGCTGC
15 TGGTGTGAGAGCAGCTGCCAGTACCAGGTGGGGGGTCAAGGTGCTGGTACTGGGGCCCCCAGCTGCCC
ACAACCCCTCTTTGTTCTCACCTGCAAAGGGTCAAGGTCAAAATGAGCCTCATCTTCTATGATCTG
GGAAGAGGTGATGATCAAGTCCCCAAGTTCAGTGTGAGGTGGACAGAGTTGGGGGGATGGCCCCCTTTTG
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20 CCTCGAGCCCCCTGAGCCAGGAGGCTCCTGGAGGAGAGCCAGGCCGGTGGGGCCGCCAAGGCTGGAGGGTC
AGCCCCAACAGGGAGCTGGGTGGGCCAGGGGGCTGGAGTGTCTACCAGCCTCTCTGGCCTATGGGGACCCA
AGAGGACACATCCCCCTTTTGCCCACTCTTCTGTGTCTATTTGTTGTTTGGTTTGTGGTGGTTTCTT
TTTTCTTTTGTTTTTCTTTTTCTTTCTTTCTTTTTTTTTTTTTTTTTTTTTTGTCACTTCGCCCA
CACAGGACAGTGGAGCCCCACCTGGTCAGTTCCACTTCCGGGCTCCCATGCACTTGCCCAAGGCGGCCTC
25 TTTGGGACGGGGATGGTTTGAGGAAACACTTTTAAAGAAAAAAGGAAGACATTGAAAGGTTTTAGTTTCT
TCCCTATCTGCATGTCTCTCATATAGAAAGCCCAGAATTAGGGGGCTAGAACTCCAGGAGAGGGTCTCCC
CGACTCATCTCTTGCTGACGGTCACCAGGATGCAGAAATAGGGAGATGGTTAGTGGGGGCCAAAGATGCC
CCCTCCAGGCCCTTCGTGGTTCCCTCCTCCGCCCCCTGCAATCTTTGGAGGAGTCAGTGCCTCACTCCAG
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30 CTGCGGGAGGCCGGGTAGCTGGAGCGAAGCGTTCCGGCTGCCCTTGCTGCTGGGTGGAGTGGAGAGGGA
GACTTCTTTTTGTTGGTTTAAATTTAAAAACACAAAGGCCATAAGAAATACGTATCTTATAATTTTTTA
ATTTTGGAGACGTTTCAATTAATGAATTGTGCACGAATGAATCTATATATATAAAATATACATATATAGC
TCTATATTTGGGGAGGGGCACTGTCTCTTTTTCTCTCATTTTAAATGAAGTGTGTTGCTTTGTAT
GTGGTCAACCATCCAGCTCCCAGCTGGCTAAACTTTGCCTCCAGTGGTCAAAGATGGGAAAAGAGTGGG
35 GTTGGCAGGAGATGGAAAACGGAGGTGCCGCCCCAGCATGGGGGGCAGGTCCCCCAGTCCACCCTGCCCC
TCCCCCTGTGGAGAAGACGCTTAGTTGGGGGTGTGGGTTTGGGCTCCATTCTGGATTCCGGCGGTTCCGGG
GGAGGGGTGGGTCTGTGCCGATTACTCTGTCTGTACGTTTGTCTGCTGCTCTTCAATATTGTATCAAC
GCCAGGAAAGGGGGGTGAAAAGCCTCTTTTACCCCCCAAATAAATTTGTACATTCCGAAGCTGA

SEQ ID NO:58

>gi|10140849|ref|NP_055107.1| chromobox homolog 6 [Homo sapiens]
MELSAVERVFAAESIIKRRIRKGRIEYLVKWKWAIKYSTWEPEENILDSRLIAAFEQKERERELYGPK
KRGPKPFTLLKARAQAEALRISDVHFSVKPSASASSPKLHSSAAVHRLKKDIRRCHMSRRPLRPDPQ
GGSPGLRPPISPFSETVRIINRKVKPREPKRNRIILNLKVIDKGAGGGGAGQGAGALARPKVPSRNRVIG
45 KSKKFSESVLRTQIRHMKFAGFALYKPPAPLVPSPGKAEASAPGGLLLAAPAAPYDARSSGSSGCP
PTPQSSDPDDTPPKLLPETVSPSPAPSWREPEVLDLSLPPEAATSKRAPPEVTAAAGPAPPTAPEPAGAS
SEPEAGDWRPEMSPCSNVVTDVTSNLLTVTIKEFCNPEDFEKVAAGVAGAAGGGGSIGASK

SEQ ID NO:59

Cytochrome C Oxidase subunit 1
>GL2_226_2_1_M13R Direction: sense
ACTTTCTCGGCCTATCCGGAATGCCCCAGCTTACTCGGACTACCCCGATGCATACACCACATGAAACATCCTAT
CATCTGTAGGCTCATTCATTTCTCTAACAGCAG

SEQ ID NO:60

>GL2_226_2_2_M13F Direction: anti-sense
CTGCTGTTAGAGAAATGAATGAGCCTACAGATGATAGGATGTTTCATGTGGTGTATGCATCGGGGTAGTCCGAGT
AACGTCGGGGCATTCGGGATAGGCCGAGAAAGT

SEQ ID NO:61

>GL2_226_2_2_M13R Direction: sense

ACTTTCCTGGCTATCCGGAATGCCCCGACGTTACTCGGACTAACCCGATGCATACACCACATGAAACATCCTATN
ATACTGTAGGCTCCATTCATTTCTCTNACAGCAGA

SEQ ID NO:62

>GL2_226_2_4_M13F Direction: anti-sense

CTGCTGTTAGAAGAAATGAATGAGCCTTACAGATGATAGGATGTTTCATGTGGTGTATGCATCGGGGTAGTCCGA
GTAACGTCGGGGCATTCGCGATAGGCCGAGAAAGT

SEQ ID NO:63

5905-7446

/gene="COX1"

/codon_start=1

/transl_table=2

/product="cytochrome c oxidase subunit I"

5881 agccattttta cctcaccccc actgatgttc gccgaccgtt gactattctc tacaaccac
5941 aaagacattg gaacactata cctattatct ggccatgag ctggagtcct aggcacagct
6001 ctaagcctcc ttattcgagc cgagctgggc cagccaggca accttctagg taacgaccac
6061 atctacaacg ttatcgtcac agcccatgca tttgtaataa tcttcttcat agtaataccc
6121 atcataatcg gaggttttgg caactgacta gttcccttaa taatcgggtg ccccgatatg
6181 gcgtttcccc gcataaacia cataagcttc tgactcttac ctccctctct cctactcctg
6241 ctcgcatctg ctatagtggg ggccggagca ggaacagggt gaacagtcta cctccctta
6301 gcagggaact actcccaccc tggagcctcc gtagacctaa ccatcttctc cttacaccta
6361 gcaggtgtct cctctatctt aggggccatc aatttcatca caacaattat caatataaaa
6421 ccccttgcca taaccaata ccaaagccc ctcttctgtc gatccgtcct aatcacagca
6481 gtcctacttc tcctatctct cccagtccta gctgctggca tcactatact actaacagac
6541 cgcaacctca acaccacctt cttcgacccc gccggaggag gagaccccat tctataccaa
6601 cactattctt gatttttcgg tcaccctgaa gtttatattc ttatcctacc aggtctcgga
6661 ataactctcc atattgtaac ttactactcc ggaaaaaaag aaccatttgg atacataggt
6721 atgggtctgag ctatgatatc aattggcttc ctagggttta tcgtgtgagc acaccatata
6781 tttacagtag gaatagacgt agacacacga gcatatttca cctccgctac cataatcatc
6841 gctatcccca ccggcgctca agtatattagc tgactcgcca cactccacgg aagcaatatg
6901 aaatgatctg ctgcagtgtc ctgagcccta ggattcatct ttcttttcac cgtagggtggc
6961 ctgactggca ttgtattagc aaactcatca ctagacatcg tactacacga caggtactac
7021 gttgtagctc acttccacta tgtcctatca ataggagctg tatttgccat cataggaggc
7081 ttcattcact gatttccctt attctcaggc tacaccctag accaaaccta cgccaaaatc
7141 catttccacta tcatattcat cggcgtaa atctaactttt tcccacaaca ctttctcggc
7201 ctatccggaa tgccccgacg ttactcggac taccctgatg catacaccac atgaaacatc
7261 ctatcatctg taggctcatt catttctcta acagcagtaa tattaataat tttcatgatt
7321 tgagaagcct tcgcttcgaa gcgaaaagtc ctaatagtag aagaaccctc cataaacctg
7381 gagtgactat atggatgcc cccaccctac cacacattcg aagaaccctg atacataaaa
7441 tctagacaaa

SEQ ID NO:64

>gi|17981855|ref|NP_536845.1| cytochrome c oxidase subunit I [Homo sapiens]
MFADRWLFSTNHKDIGTLYLLFGAWAGVLGTALSLIRAE LQPGNLLGNDHIYNVIVTAHAFVMIFFMV
MPIMIGGFGNWLVLPLMIGAPDMAFPRMNNMSFWLLPSSL LLLLASAMVEAGAGTGWTVPPLAGNYSHPG
ASVDLTIFSLHLAGVSSILGAINFITTIINMKPPAMTQYQTPLFVWSVLITAVLLLSLPVLAAGITMLL
TDRNLNTFFDPAGGGDPILYQHLFWFFGHPEVYIILPGFGMISHIVTYYSQKKEPFYMGVMVWAMMSI
GFLGFIWVAHMFVTGMDVDTRAYFTSATMIIAIP TGVKVFWSLATLHGSNMKWSAAVLWALGFIFLFTV
GGLTGIVLANSSLDIVLHDTYYVVAHFHYVLSMGAVFAIMGGFIHWFPLFSGYTLDQTYAKIHFTIMFIG
VNLTFPPQHFLGLSGMPRRYSYDPDAYTTWNILSSVGSFISLTAVMLMIFMIWEAFASKRKVLMVEEPSM
NLEWLYGCPPPYHTFEPPVYMK

SEQ ID NO:65

Delta-5 Fatty Acid Desaturase (FADS1; FADS5)

>GL1_10_3_G3F1 Direction: sense

GGCCTGAACTGNACTGAGCAGCACCGCACANAGGAGGAAGGGCAAAAAGGACGTCCCAAAGACCCAAAGGGTGAG
CCAGNCTGNACCATCCAGCAGCAAGATGTGCAGACAGGTACAGNAGGAAGAAACATGGTTGGCCTTCATGAGCC

CCATCCGCTCCACTGTGGNCCGCACTCCCGGAACCTCATCTGTCAGCTCTTTATTCTTGGTGGGNTCAAAGCTG
GGCTGNTCTGGAGACAGTTCTCCAATCAGGAGAGAGTTTCATATACTTCTTCACAAGGCCCTTGTGGATGTGGAAG
GCCACAAAGGGATCCGTGGNATCCTGNC CGNGTAGTGGCTGATGANCCGGGAGCCCCCTGNATGCCGGCGGAGT
GAACTCGCTGATGTTGTACACCTTACGGTCGATCACTANCCACCGCTCCT

SEQ ID NO:66

>GL1_10_3_G3R1 Direction: anti-sense

CAGACGCTCAAGGATGCGAGGAGCGGTGGCTAGTGATCGACCGNTAAGGTGTACAACATCAGCGAGTTCACCCGC
CGGCATCCAGGGGGCTCCCGGGTCATCAGCCACTACGCCGGNAGGATGCCACGGATCCCTTTGTGGCCTTCCAC
ATCAACAAGGGCCTTGCTGAAGAAGTATATGAACTCTCTCCTGATTGGAGAAGTGTCTCCAGAGCAGCCCAGCTT
TGAGCCACCAAGAATAAAGAGCTGACAGATGAGTTCCGGGAGCTGCGGGCCACAGTGGAGCGGATGGGGCTCAT
GAAGGCCAACCATGTCTTCTTCTGCTGTACCTGCTGCACATCTTGCTGCTGGATGGTGCAGCCTGGCTCACCTT
TTGGGTCTTTGGGACGTCCTTTTGGCCCTTCTCCTCTGTGCGGTGCTGCTCAGTGCAGTTCAGGCC

SEQ ID NO:67

delta5-Fatty acid desaturase>

ATGGCCCCGACCCGTTGGCCGCCGAGACCGCGGCTCAGGGACTTACCCC
GCGCTACTTCACCTGGGACGAGGTGGCCAGCGCTCAGGGTGCAGGAGC
GGTGGCTAGTGATCGACCGTAAGGTGTACAACATCAGCGAGTTCACCCGC
CGGCATCCAGGGGGCTCCCGGGTCATCAGCCACTACGCCGGGAGGATGC
CACGGATCCCTTTGTGGCCTTCCACATCAACAAGGGCCTTGTGAAGAAGT
ATATGAACTCTCTCCTGATTGGAGAAGTGTCTCCAGAGCAGCCCAGCTTT
GAGCCACCAAGAATAAAGAGCTGACAGATGAGTTCCGGGAGCTGCGGGC
CACAGTGGAGCGGATGGGGCTCATGAAGGCCAACCATGTCTTCTTCTGCTG
TGTACCTGCTGCACATCTTGCTGCTGGATGGTGCAGCCTGGCTCACCTTT
TGGGTCTTTGGGACGTCCTTTTGGCCCTTCTCCTCTGTGCGGTGCTGCT
CAGTGCAGTTCAGGCCAGGCTGGCTGGCTGCAGCATGACTTTGGACACC
TGTCGGTCTTCAGCACCTCAAAGTGGAACCATCTGCTACACCATTTTGTG
ATTGGCCACCTGAAGGGGGCCCCCGCCAGTTGGTGGAAACCACATGCACCT
CCAGCACCATGCCAAGCCCAACTGCTTCCGCAAAGACCCAGACATCAACA
TGCATCCCTTCTTCTTGGCCTTGGGGAAGATCCTCTCTGTGGAGCTTGGG
AAACAGAAGAAAATTATATGCCGTACAACCACCAGCACAAATACTTCTT
CCTAATTGGGGCCCCGGCCTTGCTGCTCTCTACTTCCAGTGGTATATTT
TCTATTTTGTATCCAGCGAAAGAAAGTGGGTGGACTTGGCCTGGATGATT
ACCTTCTACGTCCGCTTCTTCTCACTTATGTGCCACTATTGGGGCTGAA
AGCCTTCTGCGGCTTTTCTTCATAGTCAGGTTCTTGGAAAGCAACTGGT
TTGTGTGGGTGACACAGATGAACCATATCCCATGCACATTGATCATGAC
CGGAACATGGACTGGGTTTCCACCCAGCTCCAGGCCACATGCAATGTCCA
CAAGTCTGCCTTCAATGACTGGTTCAGTGGACACCTCAACTTCCAGATTG
AGCACCATCTTTTCCACGATGCCTCGACACAATTACCACAAAGTGGCT
CCCTGCTGCGAGTCTTGTGCGCAAGCATGGCATAGAGTACCAGTCCAA
GCCCCTGCTGTGACGCTTTCGCCGACATCATCCACTCACTAAAGGAGTCAG
GGCAGCTCTGGCTAGATGCCTATCTTCACCAATAA

SEQ ID NO:68

>gi|14141179|ref|NM_013402.3| Homo sapiens fatty acid desaturase 1 (FADS1), mRNA

TCCACTCCTGGAGCCCCGCGGACCCGAGCACGCGCCTGACAGCCCCCTGCTGGCCCCGGCGCGCGGCGTCCG
CAGGCCAGCTATGGCCCCGACCCGGTGGCCGCCGAGACCGCGGCTCAGGGACCTACCCGCGCTACTTC
ACCTGGGACGAGGTGGCCCGAGCGCTCAGGGTGCAGGAGCGGTGGCTAGTGATCGACCGTAAGGTGTACA
ACATCAGCGAGTTACCCGCGGCATCCAGGGGGCTCCCGGGTCATCAGCCACTACGCCGGGAGGATGC
CACGGATCCCTTTGTGGCCTTCCACATCAACAAGGGCCTTGTGAAGAAGTATATGAACTCTCTCCTGATT
GGAGAAGTGTCTCCAGAGCAGCCCAGCTTTGAGCCCACCAAGAATAAAGAGCTGACAGATGAGTTCCGGG
AGCTGCGGGCCACAGTGGAGCGGATGGGGCTCATGAAGGCCAACCATGTCTTCTTCTGCTGTACCTGCT
GCACATCTTGCTGCTGGATGGTGCAGCCTGGCTCACCTTTGGGTCTTTGGGACGTCCTTTTGGCCCTT
CTCCTCTGTGCGGTGCTGCTCAGTGCAGTTCAGGCCAGGCTGGCTGGCTGCAGCATGACTTTGGGCACC
TGTCGGTCTTCAGCACCTCAAAGTGGAACCATCTGCTACATCATTTTGTGATTGGCCACCTGAAGGGGGC
CCCCGCCAGTTGGTGGAAACCATGCACCTCCAGCACCATGCCAAGCCCAACTGCTTCCGCAAAGACCCA
GACATCAACATGCATCCCTTCTTCTTGGCCTTGGGGAAGATCCTCTCTGTGGAGCTTGGGAAACAGAAGA
AAAAATATATGCCGTACAACCACCAGCACAAATACTTCTTCTAATTGGGGCCCCAGCCTTGCTGCCTCT

CTACTTCCAGTGGTATATTTTCTATTTTGTATCCAGCGAAAGAAGTGGGTGGACTTGGCCTGGATGATT
ACCTTCTACGTCCGCTTCTTCTCCTCCTTATGTGCCACTATTGGGGCTGAAAGCCTTCTTGGGCCTTTTCT
TCATAGTCAGGTTCTTGGAAAGCAACTGGTTTGTGTGGGTGACACAGATGAACCATATTTCCCATGCACAT
TGATCATGACCGGAACATGGACTGGGTTTCCACCCAGCTCCAGGCCACATGCAATGTCCACAAGTCTGCC
5 TTCAATGACTGGTTCAGTGGACACCTCAACTTCCAGATTGAGCACCATCTTTTTTCCACGATGCCTCGAC
ACAATTACCACAAAGTGGCTCCCTGGTGCAGTCTTGTGTGCCAAGCATGGCATAGAGTACCAGTCCAA
GCCCCGTGCTGTCAGCCTTCGCGGACATCATCCACTCACTAAAGGAGTCAGGGCAGCTCTGGCTAGATGCC
TATCTTCCACCAATAACAACAGCCACCCTGCCAGTCTGGAAGAAGAGGAGGAAGACTCTGGAGCCAAGGC
AGAGGGGAGCTTGAGGGACAATGCCACTATAGTTTAATACTCAGAGGGGGTGGGTTTGGGGACATAAAG
10 CCTCTGACTCAAACCTCCTCCCTTTTATCTTCTAGCCACAGTTCTAAGACCCAAAGTGGGGGGTGGACACA
GAAGTCCCTAGGAGGGAAGGAGCTGTGGGGCAGGGGTGTAAATTATTTCTTTTCTAGTTTGGCAGAT
GCAGGTAGTTGGTGAACAGAGAGAACCAGGAGGGTAAACAGAAGAGGAGGACCTACTGAACCCAGAGTCA
GGAAGAGATTTAACACTAAAATTCCTCATGCGGGCGTGGTGGCACGCGCTGTAATCCCAGATACCC
AGGAGGCTGAGGCAGGAGAATCGCTTGAACCGGGGAGGTGGAGGTTGCAGTGAGCTGAGATCACGCCATT
15 GTACTCCAGCCTGGGCGACAGAGCAAGACTCCATTTCAAAAAAAAAAAAAAAAAATCCACTCATATAAAAGG
TGAGCTCAGCTCACTGGTCCATTTCTCAGTGGCTTCTCCATCTCATTGCAAACCTCAGAGGGGATAAGG
CAGTTGAACCTGATGAGCAAGAATTATAACAGCAAGGAAACATTAATGCTTAGAATTCTGAGATCCAGCA
CAACTCAGTCTGTGGGAGCTCAGCTCGCTGCCAGGGATAGGTATGACCTATGTCTGCCTTAGGCTGCTG
GGAGATGCCATTCTCAGTTTCAAGAGCAGGCAGGGCAAAGGTCAAGACTGTGGTATTGGGGTCTTTTGG
20 CTCTGAAGGATCCTGGAACTGATTTTGGTTTATCCCTCCAGGGTCTAAAGAGAACAAGAGGTGCTA
GCTCTTACCAAAACAGATGGTAGAGAGAGTTGCTGGCTATTAAAGAGCTCTTTCATCTTTAATTCACC
TCTTCTTTTACCTCTTTAACCCTCCTCAGGAACAGAACACTTCTAGGACTGGGGGTCTTTAGGCTCCA
TAAGCAAGTGAGCAGATGGGACAAGTTAGTCTTTTCTCCCTAGAAAACAAAGGGGATGCCCAGTTGGTTCC
CTTTGCTTCCCAACCTAAAATTTCAAGTTTAATAAAATAGCAATTAGCAGAAGTGACCAAAATTGGGAGAT
25 AATTATCAGTCATGAGGAAAGACACAGATTTTCGGTCTATAAGAATGTAAGGGCTATAAGTAGAACTTTC
TATAACCTAAATGATGTTATAGAATTATTTTTGAGCAGGAGCAGAAAGATTAAATATGATCACTTCATAC
TTCTAAATCAGAAATAGGAAGATTAAACCACAGAACAGTTTGTGATTTCTATTGCTGTAGCTAGGTATC
TTACTCTGTCCACTCTTGTTCAGTATCTAATCTTCTGGAAACCAATAGGCTTTAGAAGAGATTATCC
TATATTTCTATCAGTATACTAATAATGTAACCTTTTAAATCATCTGGTTTTTAAAGATAAACAGTTTA
30 GCCCATCTCTCCAGAGAGCAAAACATAGGAATATGACTCAGGAGCCTCCTAGGGCTTATCATCAGCCCTCA
CACCCGCTTCCCCCTCAACCCACAGCCTTTGCTTCCAGGTGGCAGGATTACTACTTTGCCCTCTTCAGCA
GCATCTACTCTAGGCATATTGATCATTTTAGACACTGGGAGAAGAGAACCTCAAACCTAGGAGGAAAAGAC
AGAGCCTCCACTTAGTTTTGGGAGGGGATGGCAGACAGTCAAGGAGATGAGCGTCTAAGGCATGTTGGG
ATAGGGTCAGATGCACCACCCATGGAGAGGTTTGTCAACACAAAGACATGGAAGGTTAGAGGTTTGTCAA
35 CAAAAGACATGGAAGGTTAGGTTTGTCAACACAAAGACATGGAAGATTAGAGGTTTGTCAACACAAAGA
CACAGGAAGAATGGGCTGCAGAAGATTAGATGTTTTCCATTGGGCACATTTTACTTAGCTGGAGAAT
AGGTTTTAAACAGCCTGGGTAGGAAATTAGAAGCAAGCTGGATGCAGTGGCTCATGCCTGTAATCCCAA
CACTTTTGGGAGGCTCCAGGAGGATCACTTGGGCCAGGAGGTCAAGCCTGCAGCGAGCTGAGATCA
CACCCTGCCTCCAGCCTGGGGTGATAGAACAAAGACCTGTCTCAAAAAAAAAAAAAAAAAACAAAAAAC
40 TTAGAATTGAGGAGTTGTACCTCCATTGGCTTCTCCTCACTCCAAATAGGTGCTGATCCTTCTATTCCTA
TTCTTTGCCACCTTTTGGGTGTGGTGTCAACAGCCTGTTTAGCCAAGTAGCTTTGGGCATAGGCTGCCCCA
ATCTGAGCAAAACACAGTGGGCTCTATTGAGCCAAGACCAAGTCTCAAAGCACCTGAACCACTGTGGC
CTTCTCAGCCTACAGCAGTGTGGTCTCTTACATGGCCACAAAGGGACACACAGTGACAAAAGGCTCGGAA
TGTTACAATGGTAAATGAGTGATCTCAAATCCACTGACAGATATAAAATAGGCTTAGAGAGGAAAAGCT
45 GCCTCTGGTCAAGTAGATCATGGCAGCATGAATTCCTCACTCACTTTTTTACAACCTCAACTTCTATGTTT
ATCTTTGTTACTTTTCACTTTTACAACCTGGCCAGAGGCATTTTTTAAATCAGGCCCAATATCAGTATT
CTTTTTGTGTGTGCCAATTTTGTATCACATCCCTATGAAGTTGAAAAATAAAGTTAATTTTGACCAAAA
AAAAAAAAG

50 SEQ ID NO:69
>gi|11181775|ref|NP_037534.2| fatty acid desaturase 1; delta-5 fatty acid
desaturase; linoleoyl-CoA desaturase (delta-6-desaturase)-like 1; delta-5
desaturase [Homo sapiens]
MAPDPVAAETAAGQPTPRYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPPGGSRVISHYAGQDATDP
55 FVAFHINKGLVKYMNLLIGELSPQPSFEPTKNKELTDEFRELRAFTERMGLMKANHVFFLLYLLHIL
LLDGAAWLTLWVFGTSFLPFLLCVALLSAVQAQAGWLQHDFGHLVSFSTSKWNHLLHHFVIGHLKGPAS
WWNHMHFQHHAKPNCFRKDPDINMHPFFALGKILSVELGKQKKKYPYNHQBHYFFLIGPPALLPLYFQ
WYIFYFVIQRKKWVDLAWMITFYVRFFLTYPVLLGLKAFLLGFFIVRFLESNWFWVTQMNHHPMHIDHD
RNMWDVSTQLQATCNVHKSANFNDWFSGLNFQIEHHLFPTMPRHNYHKVAPLVQSLCAKHGIEYQSKPLL
60 SAFADIHSLKESGQLWLDAYLHQ

SEQ ID NO:70

Dynactin 6, p27 subunit

>gi|18426895|ref|NM_006571.2| Homo sapiens novel RGD-containing protein (WS-3), mRNA

5 CAACCCTGCCAGGCTCTCCAATCGCATGTGGAATTATCGCTCTACCCAGGCGGTGGTGTGCGATCTACGTT
CCAATTGGGGCCGTACCATGGCGGAGAAGACTCAAAAGAGTGTGAAGATTGCTCCTGGAGCAGTTGTATG
TGTAGAAAGTGAAATCAGAGGAGATGTAAGTATCGGACCTCGGACAGTGATCCACCCTAAAGCAAGAATT
ATTGCGGAAGCCGGGCCAATAGTGATTGGCGAAGGGAACCTAATAGAAGAACAGGCCCTTATCATAAATG
10 CTTACCCAGATAATATCACTCCTGACACTGAAGATCCAGAACCAAAACCTATGATCATTGGCACCATAA
TGTGTTTGAAGTTGGCTGTTATTTCCCAAGCCATGAAGATGGGAGATAATAATGTCATTGAATCAAAAGCA
TATGTAGGCAGAAATGTAATATTGACAAGTGGCTGCATCATTGGGGCTTGTGCAACCTAAATACATTTG
AAGTCATCCCTGAGAATACGGTGATCTATGGTGCACTGCCTTCGTCGGGTGCAGACTGAGCGACCGCA
GCCCCAGACACTACAGCTGGATTTCTTGATGAAAATCTTGCCAAATTACCACCACCTAAAGAAGACTATG
15 AAAGGAAGCTCAACTCCAGTAAAGAACTAAGAACAGTGTATAACATGAAGATAACATTTTGTCTTTGACC
ACTGTCTTTTGAATGGGCCCACAGTGTTTATGTACTCTTAACAACCTACAGAATAATACATGTTTCACTTT
ATTTTGTAAAATTGGGTTGAGAGGAACTAATGGAGTTTCATTGTAACTGTCTTTGTAAATTTATATAAA
TGTATTATTTTCTATATCCTTGGTTCTTTTCTGATAATTTACAGATTTAGCTTTTCTTTGTTATATAA
ACTGCTAGCCACAATTTTAGTTATGTAAAAGGCTACCCTTGACAAGAAAAGACATACTGTCATGTATTT
20 ATATTCATAGCATAGACTAACTGAATAAAAATGCTGATAACAGGACCTTTAAAAAAAAAAAAAA

SEQ ID NO:71

>gi|5730116|ref|NP_006562.1| novel RGD-containing protein [Homo sapiens]

MAEKTQKSVKIAPGAVVCVESEIRGDTVIGPRTVIHPKARIIEAGPIVIGEGNLIEEQALIINAYPDNI
25 TPDTEDEPEPKPMIIGTNNVFEVGCYSQAMKMGDNNVIESKAYVGRNVILTSGCIIGACCNLNTFEVIPEN
TVIYGADCLRRVQTERPQPQTLLQDLFLMKILPNYHHLKKTMTKGSSTPVKN

SEQ ID NO:72

Elongation factor 1 alpha (EF1 α)

>GL1_34_LOW_3_G3F1 Direction: sense

30 ACTGTNCCTGCTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGATATGGTGGTCACCTTTGCTCCAGCTCAAC
GTTACAACGGAAGTAAAATCTGTGCGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATGTGGGC
TTCAATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTGCTGGCAACGTNGCTGGTGACAGCAAAAATGACCCACCA
ATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCC

35 SEQ ID NO:73

>GL1_34_LOW_3_G3R1 Direction: anti-sense

GGCGCTTATTTGGCCTGGATGGTTCAGGATAATCACCTGAGCAGTGAAGCCAGCTGCTTCCATTGGTGGGTCATT
TTTGCTGTCAACAGCAACGTTGCCACGACGAACATCCTTGACAGACACATTCTTGACATTGAAGCCCACATTGTC
CCCAGGAAGAGCTTCACTCAAAGCTTCATGGTGCATTTGACAGATTTTACTTCCGTTGTAACGTTGACTGGAGC
40 AAAGGTGACCACCATAACCGGTTTGAGAACACCAGTCTCCACTCGGCCAACAGGAACAGT

SEQ ID NO:74

>GL1_34_LOW_4_G3F1 Direction: sense

45 ACTGTTCCCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTT
ACAACGGAAGTAAAATCTGTGCGAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATGTGGGCTTC
AATGTCAAGAATGTGTCTGTCAAGGATGTTTCGTGCTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATG
GAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCC

SEQ ID NO:75

50 >GL1_34_LOW_4_G3R1 Direction: anti-sense

GGCGCTTATTTGGNCTGGATGGTTCAGGATAATCACCTGAGCAGTGAAGCCAGCTGCTTCCATTGGTGGGTCATT
TNTGNTGTCACCAAGCAACGTTGCCACGCAACATCCTTGACAGACACATTCTTGACATTGAAGCCCACATTGTC
CCCAGGAAGAGCTTCACTCAAAGCTTCATGGTGCATTTGACAGATTTTACTTCCGTTGTAACGTTGACTGGAGC
55 AAAGGTGACCACCATAACCGGTTTGAGAACACCAGTCTCCACTCGGCCAACAGGAACAGT

SEQ ID NO:76

>gi|20127674|ref|NM_001402.3| Homo sapiens eukaryotic translation

elongation factor 1 alpha 1 (EEF1A1), mRNA

60 GGCACGAGGGTTTGCCGCCAGAACACAGGTGTCGTGAAAACCTACCCCTAAAAGCCAAAATGGGAAAGGAA
AAGACTCATATCAACATTGTCTCATTTGGACACGTAGATTGGGGCAAGTCCACCACTACTGGCCATCTGA

TCTATAAATGCGGTGGCATCGACAAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAA
GGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGAT
ATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACT
TTATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCCTGATTGTTGCTGCTGGTGTGG
5 TGAATTTGAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGT
GTGAAACAATAATTGTCGGTGTAAACAAAATGGATTCCACTGAGCCACCCCTACAGCCAGAAGAGATATG
AGGAAATTGTTAAGGAAGTCAGCACTTACATTAAGAAAATTTGGCTACAACCCCGACACAGTAGCATTGT
GCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGG
10 AAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACCACGCTGCTTGAGGCTCTGGACTGCATCCTACCAC
CAACTCGTCCAAGTACAAGCCCTTGCCTGCTCTCCAGGATGTCTACAAAATTTGGTGGTATTGGTAC
TGTTCTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAAC
GTTACAACGGAAGTAAAATCTGTGCAAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATG
TGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCGTCTGGCAACGTTGCTGGTGACAGCAAAAA
TGACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGC
15 CCCGGCTATGCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGTCTGAGCTGAAGGAAA
AGATTGATCGCCGTTCTGGTAAAAGCTGGAAGATGGCCCTAAATTTCTGAAGTCTGGTGTATGCTGCCAT
TGTTGATATGGTTCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCTGCTTT
GCTGTTCTGTATATGAGACAGACAGTTGCGGTGGGTGTCTCAAAAGCAGTGGACAAGAAGGCTGCTGGAG
CTGGCAAGGTACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCAC
20 CCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTTGGCCATTTAAGTTTAGTA
GTAAAAGACTGGTTAATGATAACAATGCATCGTAAAACCTTCAGAAGGAAAGGAGAATGTTTTGTGGACC
ACTTTGGTTTTCTTTTTTTCGTGTGGCAGTTTAAAGTTATTAGTTTTTAAATCAGTACTTTTTAATGGA
AACAACCTTGACCAAAAATTTGTACAGAATTTTGAAGCCATTAAGGAGTTAAATGAGAAAAA
AAAAA
25 AAAAAA

SEQ ID NO:77

>gi|4503471|ref|NP_001393.1| eukaryotic translation elongation factor 1
alpha 1 [Homo sapiens]
30 MGKEKTHINIVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAEMGKGSFKYAWVLDKLKAERERG
ITIDISLWKFETSKYYVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTRHALLA
YTLGVKQLIVGVNKM DSTPEPPYSQKRYEEIVKEVSTYIKKIGYNPDVAFVPI SGWNGDNMLEPSANMPW
FKGWKVT RKDGNASGTTLLEALDCILPPTRP TDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTF
APVNVTTTEVKS VEMHHEALSEALPGDNVGFNVKNSVKDVRRGNVAGDSKNDPPMEAAGFTAQVIILNHP
35 GQISAGYAPVLDCHTAHIACKFAELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVP GKPMCVESFSDYPP
LGRFAVRDMRQTVAVGVIAVDKKAAGAGKVTKSAQKAQKAK

SEQ ID NO:78

Elongation factor 4 gamma (ElF4γ)
40 >GL1_3_1_G3F1 Direction: sense
GTCCAACCTCAAAGATATGGGAGAGGATTTGGAGTGCCTCTGTCTAGATAATGAGGACAGTGGGACCTAGATTAGAC
CATGAACGAGCCAAGTCCTTAATGGATCAGT

SEQ ID NO:79

>GL1_3_1_G3R1 Direction: anti-sense
45 ACTGATCCATTAAAGACTTGGCTCGTTCATGGTCTAATCTAGGTCCCACTGGTCCTCATTATCTGACAGAGGCAC
TCCAAATCCTCTCCCATATCTTTGAGTTGGAC

SEQ ID NO:80

>GL1_3_2_G3R1 Direction: anti-sense
50 ACTGATCCATTAAAGACTTGGNTCGTTCATGGTCTAATCTANAGTCCCACTGGTCCTCATTATCTGACAGGAGAG
CACTCCAAATCCTCTCCCATATCTTTGAGTTGGAC

SEQ ID NO:81

>gi|4503538|ref|NM_001418.1| Homo sapiens eukaryotic translation initiation
factor 4 gamma, 2 (EIF4G2), mRNA
55 CAGCAGTGAGTCGGAGCTCTATGGAGGTGGCAGCGGTACCGAGTGGCGGCTGCAGCAGCGACTCCTCTG
AGCTGAGTTTGAGGCCGTCCCCGACTCCTTCCCTCCCCCTTCCCTCCCCCTTTTTTTTGTTCCTGTTCCC
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60 CTCGGTGAAGGTATTTCAATTTCTCTGCTCCCTCCCTCCCAACCCATCTATTAAATATTATCTTTTGA

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5 ANEAVNGVREMRA PKHFLPEMLSKV IILSLDRSDEDEK EKASSLISLLKQEG IATSDNFMQAF LNVL DQCP
KLEVDIPLVKSYLAQFAARAISELVSI SELAQPLESGTHFPLFLLCLQQLAKLQDREWLTEL FQQSKVN
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10 SEQ ID NO:83

Filamin A

>GL3_11C_PCR_G3F1 Direction: sense

ACATCCAGGACACGGTGATGGCACGCACACCATTACCTACATTCCCCTCTGCCCCGGGGCCTACACCGTCACCAT
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15 SEQ ID NO:84

>GL3_15A_2_M13R Direction: anti-sense

TGCCGTACTTGATGGTGACGGTGTAGGCCCCGGGGCAGAGGGGAATGTAGGTAATGGTGTGCGTGCCATCACCGT
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20 TCGTCCATGCCGAGAGAAGGGCGAATTCTTGAGATATNCATCACACTGGCGGGCGCTCGAGC

SEQ ID NO:85

>GL3_32C_PCR_G3F1 Direction: sense

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25 AAGTACGGCACCGNAGAACCAGCACAGTGGTNAGATAGATAAAGCGGCCGCTCGACTAGTCTGAGGTCTGAATA
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AA
AAAAA

30 SEQ ID NO:86

>gi|4503744|ref|NM_001456.1| Homo sapiens filamin A, alpha (actin binding
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SEQ ID NO:87

>gi|4503745|ref|NP_001447.1| filamin 1 (actin-binding protein-280); filamin
35 A, alpha (actin-binding protein-280); filamin 1; actin-binding protein-280
[Homo sapiens]
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45 IGRSPFEVKVGTCEGNQKVRWAGPGLGGVVGKSADFVVEAIGDDVGTGLGFSVEGPSQAKIECDDKGDGS
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 LVSNHSLHETSSVFVDSLTKATCAPQHGA PGPGPADASKVVAKGLGLSKAYVGQKSSFTVDCSKAGNNML
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SEQ ID NO:88

Gα13 protein

>GL2_46_3_M13R Direction: sense

CCGCGAGGGCAGCGCGCGCGCAAGATGGCGGACTTCCTGCCGTCGCGGTCCGTGCTGTCCGTGTGCTTCCCCGG
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SEQ ID NO:89

>gi|5729847|ref|NM_006572.1| Homo sapiens guanine nucleotide binding
 protein (G protein), alpha 13 (GNA13), mRNA

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SEQ ID NO:90

>gi|5729848|ref|NP_006563.1| guanine nucleotide binding protein (G
 protein), alpha 13; guanine nucleotide binding protein, alpha-13 [Homo
 sapiens]

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SEQ ID NO:91

HOXB2

>GL3_11D_1_M13R Direction: sense

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SEQ ID NO:92

>GL3_21C_1_M13F Direction: N/A

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TGGA

SEQ ID NO:93

>GL3_11D_1_M13F Direction: anti-sense

AAAANGTATAGACTCACTATAGTGGCGAATTGGNCCATCTAGATGCATGCTCGAGCGGCCCGCCAGGTGTGATGG
ATATCTGCAGAAATTGCTGCCGCTTACGACAGTCAGTGAGTATCAGACCTCAGAGCTAGATCGAGCGGCCGCTTTA
TCTATCTAACCACTGTGCTGGGTTCGTGCGGNCCCCGCTAGAGTTTAAATGTATTCCTGAGATTTCACTGGACAGG
AGTCTACCAAACGGAATTTTCTGTGTGAATTTTAAAGATAACCGAGTGCCCAATATTTTAGAACGAAGAAGAA
AGGGAGTGGATTAAACGCTAAGTTTCAGTAATACNTGAAGTTTTTAGCAAAAGCGACATAAGTTCTATGGCGACT
GAGGGGTGGGAGAGGCTCGACGNNTTTNACCAAGTAGACGGGCCAAGGAAGGCGCGNGGGGTCCGGAAACANGG
GACCCGGGGCAGGGGGAGGGGAAAAACCAGGGTTACAGCGNGAAAAACCTGGCCAAGGACTACCCGGAACGTAT
GAGGGCCAAACAAAAGAAAGGCCGGATTAAACCTATGGGGGATTGGAAAAAATATCCCAAAGGGCTTCTCTAT
ATCCCCCTCCGGGGGAAAAAACACAGGGGGGAAACCCCGGGAGGCCCTATGGATCCAGGACACGAAAGCGAA
AACCCCTCGGGTAAGAGAGCCCTAAGGGGGGA

SEQ ID NO:94

>GL3_27D_2_M13R Direction: anti-sense

CCCCCTAGAGTTTAAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTCTGTGTGAATTTT
AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG
AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTCCAGTAGACGGCCAAGGAG
CGCGGGGGTCCGAAAGGACCGGGAGGAGGAAACAGGTTAGGGAACTGCAGGTCGATGGCAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGGCTGTGAGAGAAACCTGTAGGCTAGGGGAGAGGCTCCG
GATAGCTGGAGACAGGAGTCGGCCGCGAAGAAGTTGAGGTGCGGAAGGAAAGGTGAATCCTGGCGCCCCGAGAAG
ACGTCTTCTGGCAATGGCCCGGGCTCCAGCCCGACGGCCCCGCGCAGCGCGCAAGCCGGGACTTCGAACGCACNC
NTGCAGCCCTCATAAGCGAACGGCATAAAAGGCCCGGGGGTTCAGCGCATTAAGGGCCCCCGGACCATCTTCC
GGGCGAGGTGAACAAGCGGGGTACCCAAGGCCGGCGAGAGGTCCCCGAGGCCATTNGACTAGGGNT

SEQ ID NO:95

>GL3_45B_3_M13F Direction: N/A

TTTGCCCTGACCCGGGCCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAAACCAAAAGCAATGGCCTGGGACTGCG
CGGAGGCTGGTGGCGCGGGGCGCGCAGGCTGCGCACGGTTTACACCAACGCGAGCTGCTGGAACCTGGAGAAG
GAATTCACCTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCTTGTGTTGACCTACCGAAAGG
CAGGTCAAAGTCTGGTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCGACCCGAGAGCCGCCGATGGG
GAGCCTGCCTGCCCCGGGAGCCCTGGAGGACATCTGCGACCCTGCCGAGGAACCTGCGGCCAGCCGGGCGGCC
CTCCGCTCGCGGGCGCGTGGGAAGCCTGCTGTACCCGCCGAGGTGGTTGCCGGGGGCC

SEQ ID NO:96

>GL3_27D_1_M13R Direction: anti-sense

CCCCCTAGAGTTTAAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTCTGTGTGAATTTT
AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG

AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTCCAGTAGACGGCCAAGGAG
CGTGGGGGTGCAAAGGACCGGGAGGAGGAAACAGGTTAGGGAACTGCAGGTGCGATGGCACAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCCTCGGAAAAAGGGACCGGGCTGTGCGAGAGAACCCTGTAGGCTAGGGGAGAGGCCTCCG
5 GATAGCTGGAGACAGGAGTCGGCCGCGAAGAAGTTGAGGTGCGGAAGGAAAGGTAATTCCTTCTCCAGTTCAGC
AGCTGCGTGTGGTGTAAAGCCGTG

SEQ ID NO:97

>GL3_45B_1_M13R Direction: sense

TTTGCCCTGACCCGGGCCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAAACCCAAAAGCAATGGCCTGGGACTGC
10 CGGAGGCTGGTGGCGGGCGGGCGCAGGCTGCGCACGGTTACACCAACACGCAGCTGCTGGAACCTGGAGAAGGA
ATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCCTTGCTGGACCTCACCGAAAGGCA
GGTCAAAGTCTGGTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGGATGGGGA
GCCTTGCCCTTGCCGGGAGCCCTTGAGGACATCTGCGACCCTGCCGAGGAACCCGCGGGCCAGCCCGGGCGGCC
15 CCTTCGCCCTCGCGGGCGGGCG

SEQ ID NO:98

>GL3_11D_3_M13R Direction: anti-sense

CCCCCTAGAGATTCTAATGTACTTCTGAGATTATCACTGGAAGGAGATCTACCAAACGGAATTTCTTCCGTGT
GAATTTTAGACAGAGATAACCGAGTGGCCATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGT
20 AATACCTGAATTTTAGCAAAAGACACATAAGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTCCAGTAGACG
GCCAAGGAGCGCGGGGTGCAAAGGACCGGGAGGAGGAAACAGGTTAGGGAAACTGCAGTCTGACTGGCACAGAG
CGTACTGGTGAAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGGCTGTGCGAGAGAACCCTGGTAGGCTAGGGG
AGAGGCCTCCGATAGCTGGAGACAGGAGTCGGCCGCGAANGAAGTTGAGGTGCGGAAGGAAAGGTGAATCC

SEQ ID NO:99

>GL3_11D_4_M13F Direction: sense

AAATTGGAAATAGACTCACTATAGGGCGAATTGGGCCCTCTAGAATGACATGCTCGAGCGGCCAGNCCAAGGTGT
GATGGATATCTGCAGAAATCTGCCCTTACGACAGTCAGTGAGTATCAGACCTCAGAGCTAGATCGTAGCGGCCG
30 TTTATCTATCTAACCACTGTGCTGGGTNTCTGCGGCCCCCGCTAGAGTTTAATTATTCCTGAGATTTCACTGGCC
AGGGAGTCTACCAACAGGGAATTTTCTGTGTGAATTTTAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGA
AGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTGAATTTTAGCAAAACACATAAGTCTATGCGACTGAGG
GTGGGAGAGGCTCGATTTTTCAGTAGACGGCCAAGGAGCGCGGGGNCGAAAGGACCGGGAGGAGGAAACAGGT
TAGGGAAACTGCAGGTGCGATGGCACAGAGCGTACTGGTGAAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGG
35 GTGTAAGAGAGAACCCTGNAAGGCCAGCGGGA

SEQ ID NO:100

>GL3_41D_1_M13R Direction: anti-sense

CCCCCTAGAGTTTAAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAGACGGAATTTTCTGTGTGAATTT
AAGAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCT
40 GAATTTTAGCAAAACACATAACGCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTGTCCAGTACGACGGCCAA
GGAGCGCGCGGGGTGCAAAGGACCGGGAGGAGGAAACAGGTTAGGGAAACTGCAGGTGCGATGGCACAGAGCGTAC
TGGTGAAAAAATCCAGCTCTACCTCGGAAAAAGGGACCGGGACNGATCGAGAGAACCCTGTAGGCTAGGGGAGA
GGCCATCCGATAGACTGGAGACAGGAGTCGGAACGCGAAGAAGTACGAGGTGNGGAAGG

SEQ ID NO:101

>GL3_41D_3_M13R Direction: anti-sense

CCCCCTAGAGTTTAAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTCTGTGTGAATTT
AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG
AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGGTGGGAGGGGCTCGATTTTCCAGTAGACGGCCAAGGAG
50 CGCGGGGTGCAAAGGACCGGGAGGAGGAAACAGGTTNAGGGAACCTGCAGGTGCGATGGCACAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCCTCGGAAAAAGGGACCGGGACNGATCGAGAGAACCCTGTAGGCTAGGGGAGAGGCCTCCG
GATAGCTGGAGACAGGAGTCGGCCGCGAAGAAGTNGAGGTGCGGAAGGAAAGCGTGAAAGTCCCTGGCACAGCCA
CCGAAGGCAAAGAACGGATCNTTTTCATNGGACAAAAATGGGACCCAGGAGCATCCCAAGCACCCGGANCGGGCG
CCCGGACGCGCAGNAGCGCAAAGACAGGGNGAACTCACGAAAGGCAGNACNTGACGACCCCATTCAAAAAG
55 GAGAGAACAANGGNATAAAAAGGGACCAGGAGAAGANCAAG

SEQ ID NO:102

>GL3_41D_4_M13R Direction: anti-sense

CCCCCTAGAGTTTAAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTCTGTGTGAATTT
60 AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG

5

>GL3 45B 1 M13F Direction: anti-sense

10

>GL3 45B 3 M13R Direction: anti-sense

20

>GL3 45B 4 M13R Direction: anti-sense

30

>GL3 27D 3 M13F Direction: N/A

40

>GL3_27D_3_M13R Direction: anti-sense

50

>GL3 27D 4 M13F Direction: N/A

60

CTCTCCCCTAGCCTACAGGGTTCTCTCGACAGCCCGGTCCCTTTTTCCGAGGAAGAGCTGGATTTTTTCACCAGT
ACGCTCTGTGCCATCGACCGTGCAGTTTCCCTAACCTGTTTCTCTCCCGTCTTTTCGACCCCGCGCTCCTT
GGCCGTCTACTGGAAAAATCGAGCCTCTCCACCCCTCAGTCGCATAGACTTATGTGTTTGGCTAAAATTCAGGTA
TTACTGAATTAGCGTTTAATCCACTCCCTTTCTTCTTCTTCTAAATATTGGGCACATCGGTTATCTTTTAAAA
5 TTCACACAGAAAAATTCGGTTAGGG

SEQ ID NO:109

>GL3_27D_4_M13R Direction: anti-sense

CCCCCTAGAGTTTAATTATTCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTTCTGTGTGAATTTT
10 AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG
AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTTCCAGTAGACGGCCAAGGAG
CGCGGGGGTTCGAAAGGACCGGGAGGAGGAAACAGGTTAGGGAAACTGCAGGTCGATGGCACAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGGCTGTGAGAGAACCCTGTAGGCTAGGGGAGAGGCCTCCG
15 GATAGCTGGAGACAGGAGTCGGCCCGGAAGAAGTTGAGGTCGGGAAGGAAAGGTGAATCCTGGCGCCCCGAGAAG
ACGTCTTCTGGCAATGGGTTTTCTTCTCTCCCTCTCTAGTCTACAGCCCGTGGCCGGGGTCAGGGCAAACCGGAG
AAACCAGCACACTGGAGCCA

SEQ ID NO:110

>GL3_21C_1_M13R Direction: anti-sense

CCCCCTAGAGTTTAATTATTCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTTCTGTGTGAATTTT
20 AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG
AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTTCCAGTAGACGGCCAAGGAG
CGCGGGGGTTCGAAAGGACCGGGAGGAGGAAACAGGTTAGGGAAACTGCAGGTCGATGGCACAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGGCTGTGAGAGAACCCTGTAGGCTAGGGGAGAGGCCTCCG
25 GATAGCTGGAGACAGGAGTCGGCCCGGAAGAAGTTGAGGTCGGGAAGGAAAGGTGAATCCTGGCGCCCCGAGAA
GACGTCTTCTAGGCAATGGCCCGGGTCAGGGCAA

SEQ ID NO:111

>GL3_41D_3_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGGAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGCGCGCAGGCTGCGCACGGTTTACACCAACACGCAGCTGCTGGAACCTGGAGAAGG
AATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCCTTGCTGGACCTCACCGAAAAGGC
AGGTCAAAGTCTGGTTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGGATGGGG
35 AGCCTGCCTGCCCCGGGAGCCCTGGAGGACATCTGCGACCCTGCCGAGGAACCCGCGGCCAGCCCGGGCGGGCCCT
TCCGCCTCGCGGGCGGCGTGGAAGCCTGCTGTCACCCGCCGAGGTGGTGCCGGGGGCTTAAGCGCGGACCCC
GGCCTTTAGCCGTTCCG

SEQ ID NO:112

>GL3_41D_4_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGCGCGCAGGCTGCGCACGGTTTACACCAACACGCAGCTGCTGGAACCTGGAGAAGG
AATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCCTTGCTGGACCTCACCGAAAAGGC
AGGTCAAAGTCTGGTTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGGATGGGG
45 AGCCATGCCTGCCCCGGGAGCCCTTGGAGGACATCTGCGACCCTTGCCGAGGAACCCGCGGGCCAGCCCGGNNCG
GCCCCATCCGCCTCG

SEQ ID NO:113

>GL3_41D_PCR_G3F1 Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGCC
50 GGAGGCTGGTGGCGGGCGGGCGCGCAGGCTGCGCACGGCTTACACCAACACGCAATTCTGGAACCTGGAGAAGGAA
TTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCCTTGCTGGACCTCACCGAAAAGGC
GTCAAAGTCTGGTTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGGATGGGGAG
CCTGCCTGCCCCGGGAGCCCTGGAGGACATCTGCGACCCTGCCGAGGAACCCGCGGGCCAGCCCGGGCGGGCCCTCC
GCCTCGCGGGCGGGCTGGGAAGCCTGCTGTCACCCGCCGAGGTGGTGCCGGGGGCTTAAGCGCGGACCCCCGG
55 CCTTTAGCCGTTTCGCTTAGAGGGCGCAGGCGCTCGAGTCCCGGCTGCGCGCTGCGCGGGGCCGGCGGGCTGGAG
CCCGGGCCATTGCCAGAAGACGTCTTCTCGGGGCGCCAGGATTACCTTTCTTCCCGACCTCAACTTCTTCGCG
GCCGACTCCTGTCTCCAGCTATCCGAGGCCTTCCCTAGCCTACAGGGGTTCTCTCGACAGCCCGGTCCCTTTT
TCCGAGGAAGAGCTGGATTTTTTACCAGTACGCTCTGTGCCATCGAC

SEQ ID NO:114

>GL3_41E_PCR_G3F1 Direction: sense

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGCGCAGGCTGCGCACGGCTTACACCAACACGCAGCTCTGGAACCTGGAGAAGGA
ATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCGTCGAGATCGCGGCCCTTGCTGGACCTACCGAAAGGCA
GGTCAAAGTCTGGTTTCAGAACC GGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGATGGGGG
GCCTGCCTGCCCCGGGAGCCCTGGAGGACATCTGCGACCCTGCCGAGGAACCCGCGGCCAGCCCGGGCGGGCCCCCTC
CGCCTCGCGGGCGGGCTGGGAAGCCTGCTGTACCCGCCGAGGTGGTGGCGGGGGCCTTAAGCGCGGACCCCCG
GCCTTTAGCCGTTTCGCTTAGAGGGCGCAGGCGCGTCGAGTCCCGGCTGCGCGCTGCGCGGGGCGGGCGGGCTGGA
GCCCCGGGCCATTGCCAGAAGACGTCTT

SEQ ID NO:115

>GL3_45B_4_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGCGCAGGCTGCGCACGGCTTACACCAACACGCAGCTGCTGGAACCTGGAGAAGG
AATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCGTCGAGATCGCGGCCCTTGCTGGACCTACCGAAAGGC
AGGTCAAAGTCTGGTTTCAGAACC GGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGATGGGG
AGCCTGCCTGCCCCGGGAGCCCTGGAGGACATCTGCGACCCTTGCCGAGGAACCCGCGGCCAGCCCGGGCGGGCCC

SEQ ID NO:116

>GL3_45B_PCR_G3F1 Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGGCGCGCAGGCTGCGCACGGCTTACACCAACACGCAGCTGCTGGAACCTGGAGAAGG
AATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCGTCGAGATCGCGGCCCTTGCTGGACCTACCGAAAGGC
AGGTCAAAGTCTGGTTTCAGAACC GGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGATGGGG
AGCCTGCCTGCCCCGGGAGCCCTGGAGGACATCTGCGACCCTTGCCGAGGAACCCGCGGCCAGCCCGGGCGGGCCCCCT
CCGCCTCGCGGGCGGGCTGGGAAGCCTGCTGTACCCGCCGAGGTGGTGGCGGGGGCCTTAAGCGCGGACCCCC
GGCCTTTAGCCGTTTCGCTTAGAGGGCGCAGGCGCGTCGAGTCCCGGCTGCGCGCTGCGCGGGGCGGGCGGGCTGG
AGCCCCGGGCCATTGCCAGAAGACGTCTTCTCGGGGCG

SEQ ID NO:117

>GL3_27D_1_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAGAAAGCAATGGCCTGGGACTGC
CGGAGGCTTTGGTTGGCGGGCGGGGCGCGCAGGCTTGGCGGCAACGGTTTTTACACCAAAACACGCAGCTGCTTGGAA
CTGGAGAAAGGAAATTAACCTTTTCTCTTCCCGAACCTTCAAACCTTTCTTTGGCGGGCCGGACTTCTTTGTCTC
TCCAGCTTATCCGGAGAGCGCTTCTCCCCATTAGCCCTAACAAAGGGTTCTCTCNGGACAGGCCCGCGGGGTCC
CCTTTTTTCCGGAGAAAGAGCTTGAATTTTCCCAACCAAGGTACGGCCCATTCGTTTGGTTGCCCCCAATTTCTGT
AGAACCCTTTGCACAAGGTTTTTCCCCCTATAAAAACCTGTGGTTTTTCCCCTTCCACCTTTCCCCGCGGGGG
TATCCCTTTTTTTCAGGAAGCCGCGCCNACAAAAGGGCTTCTTATTTTGGGCCCCGGTGTACTCTTTAGCGTGTGG
GAAAACAGAAATTCGTCGGGAAGGCCCTTCTTCCACAAACCCCCATTTCNAGAGGTCCGGGGCAAGATTTAGAAA
CTTTATTGGACTATGATTTGTGTTGAGGGCCCTTAAACACAAATTTTCAAGGGGATTATTTT

SEQ ID NO:118

>GL3_27D_2_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGCACTGC
CCTGGCGCTTTGGGAAGCGTGTCTACCCGTCGCGAGGGTGGATGCCGTGGGGTCTATGAAGCTGCGGACCCC
CGGTCTTTAGACCGTACGCTTAGAGCGGGCGGACAGGCNCGTCGAGGTCCCGGCTGCGAACAGCGCGGAGCCCCGGG
CNGCATGAAGCCTCGTGTNCNAATTTNCCAAGAAATGGAAGGGTTCTTACCCTTCNGAGGCGCGGCCCAAGNGTA
CTTCTTACCCCTGTGTTTCCCTTTTCCCCGAAACCCTCTCGAAGTCTTTCTTTACGGGCGNGGCCAGANACTC
CGTTGTTTCTACCTTANGGATTACANCTGAGAAGACCTTTTNCACGCCTCNTTGGAGGCTCACTGTAAACNNG
TGGGAGGGTTNGTCTCCGTTCTTNCGGGGACCTAAGCGGGCCCCGCTGGGCGAACCGCGGTTTTTTTAAACCTCA
CCGGGAGAAAGNAGACAAAANGACAAAGGGTCTTTTGAGGAAGATTCCATCTTTNCACNACCCGTATAGATTAGT
TAACGGGTCTCCCTGTGCTTCGCCACATATTTAAGTACCGGCTGTGGGCGAAGCGTTCTTGGCCCNCAATTA
CACAGTCCNCTTTGTGATATAACCCNCTTTCCACTCTTACCCGNGCGGGGACTCCCACTTTTTTTT

SEQ ID NO:119

>GL3_41D_1_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGGCGCGCAGGCTGCGCNACGGTTACACTCAACTACGCAGCTGCTGGAACCTGGAGA
AGGAATTTCCACTTTAATAAGTACCTTGTGTCCGGGCCACAGCCGGCGGTTCAGAGATCNGCGGGCCTTTGCCTGG

ACCCCTTCAGCCCGAAAAGGGCAAGGTCNAAGAGGCTCATAGGGTGTCCAGAGACNCGNGGCGGCCAATTGAAGA
GGCAACGAGAGGGCCGGCCAAGGAACGGCAGCAACCCGGAAGAAGGCCCGGCCGNGGCATTGGGGGGGAAGCCTT
NGCCCTTGGCCCCGGTGGTGAAGGTCCGCTTTGGGAANGGGAGCATATTCTTNGCGAAACGCTTGTGTCNAGAA
GGGTAGAAACCCCGTGACGGGGGCCAAGGGCGCCCCGGGGGCGGCGGCCCCCTTTCCGGACCCATTTCGGGGCC
GGGGTAGCCGGGNCAGTTG

SEQ ID NO:120

gji|4504464|ref|NM_002145.1| Homo sapiens homeo box B2 (HOXB2), mRNA
GAATTCGGGGGGGGGGTCCCTTCCGATCCTCCCTCCTGACGCCCCCCCCAGCAGCCCCCTCCCCACCAT
TGAAAGCCATGAATTTTGAATTTGAGAGGGAGATTGGGTTTATAAACAGCCAGCCGTCGCTCGCCGAGTG
TCTGACTTCCCTTCCCCGCTGTCTTGGAGACATTTCAAACCTTCATCAATCAAGGAGTCGACATTAATTCCCT
CCTCCTCCTCCTTTTCGAGCAAACCTTCCCCAGCCTCCAGCCCGCGCCTCCACCCTTCAGAGACCCAGGA
GCCAAAAGCGAGCCGAAGATGGCGCTGCTTGCCTGCCACCGCGCCGCGCCACTCCCCGCTGCCCCCCC
GGCCCCCGAGTTCCCTTGGATGAAAGAGAAGAAATCCGCCAAGAAACCCAGCCAATCCGACACGTCCTCT
TCTCCGGCCGCTCCGCCGTTCCGGCCTCCGGGGTCGGATCGCCTGCAGATGGCCTGGGACTGCCGGAGG
CTGGTGGCGGCGGGGCGCGCAGGCTGCGCACGGCTTACACCAACACGCAGCTGCTGGAACCTGGAGAAGGA
ATTCACATTTAATAAGTACCCTGTGCGGCCACGCCGCGTCGAGATCGCGCCTTGCTGGACCTCACCAGAA
AGGCAGGTCAAAGTCTGGTTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCAGCACCCGAGAGCCGC
CGGATGGGGAGCCTGCCTGCCCGGGAGCCCTGGAGGACATCTGCGACCCTGCCGAGGAACCCGCGGCCAG
CCCCGGCGCCCCCTCCGCCCTCGCGGGCGGGCTGGGAAGCCTGCTGTACCCGCGCGGAGGTGGTGCCGGGG
GCCTTAAGCGCGGACCCCGGCCCTTACCGCTTCGCTTAGAGGCGCAGGCGCGTCGAGTCCCGGCTGCG
CGCTGCGCGGGGCCGGCGGGCTGGAGCCCGGGCCATTGCCAGAAGACGCTCTTTCGGGGCGCCAGGATTTC
ACCTTTCCCTTCCCGACCTCAACTTCTTCGCGGCCGACTCCTGTCTCCAGCTATCCGGAGGCCCTCTCCCCCT
AGCCTACAGGGTTCTCTCGACAGCCCGTCCCTTTTTCCGAGGAAGAGCTGGATTTTTTACCAGTACGC
TCTGTGCCATCGACCTGCAGTTTCCCTAACCTGTTTCTCCTCCCGGTCCTTTCGACCCCCGCGCTCCTT
GGCCGTCTACTGGA AAAATCGAGCCTCTCCACCTCAGTCGCATAGACTTATGTGTTTTGCTAAAATTC
AGGTATTACTGAATTAGCGTTTAATCCACTTCTCTTTCTTCTTCTTCTAAAATATTGGGCACTCGGTTATC
TTTTAAAATTACACAGAAAAAATCCGTTTGGTAGACTCCTTCCAATGAAATCTCAGGAATAATTAACT
CTAGGGGGGACTTTCTTTAAAATAACTAGAGGGACCTATTTTCTCTTTTATGTTTTAGACTGTAGATT
ATTTATTTAAAATTCTTTAATAATAGGAAAAGGGGAAAGTATTTATTGTAC

SEO ID NO:121

>gi|4504465|ref|NP_002136.1| homeo box B2; Homeo box-B2 [Homo sapiens]
MNFEREIGFINSQPSLAECTLSFPAVLETFQTSSIKESTLIPPPPPFQTFPSLQPGASTLQRP RSQK
RAEDGPALPPPPPPPLPAAPPAPAEFFWMKEKKS AKKPSQSATSPPSPAASAVPASGVGSPADGLGLPEAGG
GGARRLR TAYTNTQLLELEKEFHFNKYLCRRRVEIAALLDLTERQVKVWFQNRMRMKHKRQTQHREPPDG
EPACPGALEDICDPAEPPAASPGGPSASRAAWEACHPPEVVPGALSADPRPLAVRLEGAGASSPGCALR
GAGGLEGPPLPEDVFSGRQDSPFLPDLNFFAADSCLQLSGGLSPSLQGS LDSPVPFSEELDFFTSTLCA
IDLOFP

SEQ ID NO:122

HSPA5

>GL2-67-2M13R Direction: N/A

CCGATGAGCCGCTTGGCGTCAAAGACCGTGTCTCGGGTTGGAGGTGAGCTGGTTCTTGGCGGCATCGCCAATC
AGACGTTCCCTTTCAGGAGTGAAGGCGACATAGGACGGCGTGATGCGGTTGCCCTGATCGTTGGCGATGATCTCC
ACGCGGCCGCTCGCGATCTAGAAC

SEQ ID NO:123

>GL2-67-5M13F Direction: N/A

GTTCTAGATCGCGAGCGGCCGCGTGGAGATCATCGCCAACGATCAGGGCAACCGCATCACGCCGTCCATATGTCGC
 CTTCACTCCTGAAGGGGAACGTTCTGATTGGCGATGCCCGCAAGAACCAGCTCACCTCCAACCCGAGAACACGGT
 CTTTGACGCCAGCGGCTCATCGG

SEQ ID NO:124

>GL2-67-5M13R Direction: N/A

CCGATGAGCCGCTTGGCGTCAAAGACCGTGTTCTCGGGTTGGAGGTGAGCTGGTTCTTGGCGGCATCGCCAATC
AGACGTTCCCTTCAGGAGTGAAGGCGACATAGGACGGCGTGATGCGGTTGCCCTGATCGTTGGCGATGATCTCC
ACGCGGCCGCTCGCGATCTAGAAC

SEQ ID NO:125

>GL2_1_A03_G3F1 Direction: sense

GTTCTAGATCGCGAGCGGCCGCGTGGAGATCATCGCCAACGATCAGTGGCAACCGCATCACGCCGTCCTATGTCG
CCTTCAC'TCCTGAAGGGGAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCACCTCCAAACCCGAGAACACGG
TCTTTGACGCCAAGCGGCTCATCTGG

SEQ ID NO:126

>GL2_1_A05_G3F1 Direction: sense

GTTCTAGATCGCGAGCGGCCGCGTGGAGATCATCGCCAACGATCAGGGGCAACCGCATCACGCCGTCCTATGTCG
CCTTCAC'TCCTGAAGGGGAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCACCTCCAAACCCGAGAACACGG
TCTTTGACGCCAAGCGGCTCATCGG

SEQ ID NO:127

HSP5>

ATGGAGGAGGACAAGAAGGAGGACGTGGGCACGGTGGTCGGCATCGACCT
GGGGACCACCTACTCCTGCGTCGGCGTGTTCAGAAGACGGCCGCGTGGAGA
TCATCGCCAACGATCAGGGCAACCGCATCACGCCGTCCTATGTCGCCTTC
ACTCCTGAAGGGGAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCAC
CTCCAACCCCGAGAACACGGTCTTTGACGCCAAGCGGCTCATCGGCCGCA
CGTGGAATGACCCGTCTGTGCAGCAGGACATCAAGTTC'TTGCCGTTCAAG
GTGGTTGAAAAGAAAATAAACCATACATTCAAGTTGATATTGGAGGTGG
GCAAACAAAGACATTTGCTCCTGAAGAAATTTCTGCCATGGTTCTCACTA
AAATGAAAGAAACCGCTGAGGCTTATTTGGGAAAGAAGGTTACCCATGCA
GTTGTTACTGTACCAGCCTATTTTAATGATGCCCAACGCCAAGCAACCAA
AGACGCTGGAACATATTGCTGGCCTAAATGTTATGAGGATCATCAACGAGC
CTACGGCAGCTGCTATTGCTTATGGCCTGGATAAGAGGGAGGGGGAGAAG
AACATCCTGGTGT'TTGACCTGGGTGGCGGAACCTTCGATGTGTCTCTTCT
CACCATTGACAATGGTGTCTTCGAAGTTGTGGCCACTAATGGAGATACTC
ATCTGGGTGGAGAAGACTTTGACCAGCGTGTATGGAACACTTCATCAAA
CTGTACAAAAAGAACGCGGCAAGATGTCAGGAAAGACAATAGAGCTGT
GCAGAAACTCCGGCGCGAGGTAGAAAAGGCCAAACGGGCCCTGTCTTCTC
AGCATCAAGCAAGAATTGAAATTGAGTCCTTCTATGAAGGAGAAGACTTT
TCTGAGACCCCTGACTCGGGCCAAATTTGAAGAGCTCAACATGGATCTGTT
CCGGTCTACTATGAAGCCCGTCCAGAAAGTGT'TGGAAGATTCTGATTTGA
AGAAGTCTGATATTGATGAAATTGTTCTTGT'TGGTGGCTCGACTCGAATT
CCAAAGATTCAAGCAACTGGTTAAAGAGTTC'TTCAATGGCAAGGAACCATC
CCGTGGCATAAACCCAGATGAAGCTGTAGCGTATGGTGTCTGTGTCAGG
CTGGTGTGCTCTCTGGTGTATCAAGATACAGGTGACCTGGTACTGCTTGAT
GTATGTCCCTTACACTTGGTAT'TGAACTGTGGGAGGTGTATGACCAA
ACTGATTCCAAGGAACACAGTGGTGCCTACCAAGAAGTCTCAGATCTTTT
CTACAGCTTCTGATAATCAACCAACTGTTACAATCAAGGTCTATGAAGGT
GAAAGACCCCTGACAAAAGACAATCATCTTCTGGGTACATTTGATCTGAC
TGGAATTCCTCCTGCTCCTCGTGGGGTCCACAGATTGAAGTCACCTTTG
AGATAGATGTGAATGGTATTCTTCGAGTGACAGCTGAAGACAAGGGTACA
GGGAACAAAAATAAGATCACAATCACCAGATGACGAGATCGCCTGACACC
TGAAGAAATCGAAAGGATGGTTAATGATGCTGAGAAGTTTGCTGAGGAAG
ACAAAAAGCTCAAGGAGCGCATTTGATACTAGAAATGAGTTGGAAAGCTAT
GCCTATTCTCTAAAGAATCAGATTGGAGATAAAGAAAAGCTGGGAGGTAA
ACTTTCCTCTGAAGATAAGGAGACCATGGAAAAAGCTGTAGAAGAAAAGA
TTGAATGGCTGGAAAGCCACCAAGATGCTGACATTGAAGACTTCAAAGCT
AAGAAGAAGGAAC'TGGAAGAAATTGTTCAACCAATTATCAGCAAACTCTA
TGGAAGTGCAGGCCCTCCCCCAACTGGTGAAGAGGATACAGCAGAACTCC
ACCACCACCACCACC

SEQ ID NO:128

>gi|21361242|ref|NM_005347.2| Homo sapiens heat shock 70kD protein 5
(glucose-regulated protein, 78kD) (HSPA5), mRNA

ACAGCACAGACAGATTGACCTATTGGGGTGT'TTCGCGAGTGTGAGAGGGGAAGCGCCGCGGCTGTATTTTC
TAGACCTGCCCTTCGCTGGTTTCGTGGCGCCTTGTGACCCCGGGCCCTGCCGCTGCAAGTCGGAAATT
GCGCTGTGCTCCTGTGCTACGGCCTGTGGCTGGACTGCCTGCTGCTGCCCCAAGTGGCTGGCAAGATGAAG

CTCTCCCTGGTGGCCGCGATGCTGCTGCTGCTCAGCGCGGCGCGGGCCGAGGAGGAGGACAAGAAGGAGG
 ACGTGGGCACGGTGGTTCGGCATCGACCTGGGGACCACCTACTCCTGCGTCGGCGTGTTCAGAACGGCCG
 CGTGAGATCATCGCCAACGATCAGGGCAACCGCATCAGCCGTCCTATGTCGCCTTCACTCCTGAAGGG
 5 GAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCACCTCCAACCCGAGAACACGGTCTTTGACGCCA
 AGCGGCTCATCGGCCGCACGTGGAATGACCCGCTCTGTGCAGCAGGACATCAAGTTCTTGCCGTTCAAGGT
 GGTGAAAAAGAAAACTAAACCATACATTCAAGTTGATATTGGAGGTGGGCAAACAAAGACATTTGCTCCT
 GAAGAAATTTCTGCCATGGTTCTCACTAAAATGAAAGAAACCGCTGAGGCTTATTTGGGAAAGAAGGTTA
 CCCATGCAGTTGTTACTGTACCAGCCTATTTAATGATGCCCAACGCCAAGCAACCAAGACGCTGGAAC
 10 TATTGCTGGCCTAAATGTTATGAGGATCATCAACGAGCCTACGGCAGCTGCTATTGCTTATGGCCTGGAT
 AAGAGGGAGGGGGAGAAGAACATCCTGGTGTGTTGACCTGGGTGGCGGAACCTTCGATGTGTCTCTCTCA
 CCATTGACAAATGGTGTCTTCGAAGTTGTGGCCACTAATGGAGATACTCATCTGGGTGGGAGAAGACTTTGA
 CCAGCGTGTCTGGAACACTTCATCAAACTGTACAAAAGAAGACGGGCAAAGATGTCAGGAAAGACAAT
 AGAGCTGTGCAGAACTCCGGCGCGAGGTAGAAAAGGCCAAACGGGCCCTGTCTTCTCAGCATCAAGCAA
 15 GAATGAAATTGAGTCTTCTATGAAGGAGAAGACTTTTCTGAGACCCTGACTCGGGCCAAATTTGAAGA
 GCTCAACATGGATCTGTTCCGGTCTACTATGAAGCCCGTCCAGAAAGTGTGGAAGATTCTGATTTGAAG
 AAGTCTGATATTGATGAAATGTTCTTGTGTTGGTGGCTCGACTCGAATTCCAAAGATTTCAGCAACTGGTTA
 AAGAGTTCTTCAATGGCAAGGAACCATCCCGTGGCATAAACCCAGATGAAGCTGTAGCGTATGGTGCCTGC
 TGTCCAGGCTGGTGTGCTCTCTGGTGATCAAGATACAGGTGACCTGGTACTGCTTGATGTATGTCCCTTT
 ACACTTGGTATTGAACTGTGGGAGGTGTCTATGACCAAACTGATTCCAAGGAACACAGTGGTGCCTACCA
 20 AGAAGTCTCAGATCTTTTCTACAGCTTCTGATAATCAACCAACTGTTACAATCAAGGTCTATGAAGGTGA
 AAGACCCCTGACAAAAGACAATCATCTTCTGGGTACATTTGATCTGACTGGAATTCCTCCTGCTCCTCGT
 GGGGTCCACAGATTGAAGTCACCTTTGAGATAGATGTGAATGGTATTCTTCGAGTGACAGCTGAAGACA
 AGGGTACAGGGAACAAAATAAGATCACAATCACCATGACCAGAATCGCCTGACACCTGAAGAAATCGA
 AAGGATGGTTAATGATGCTGAGAAGTTTGCTGAGGAAGACAAAAAGCTCAAGGAGCGCATTTGATACTAGA
 25 AATGAGTTGGAAGCTATGCCTATTCTCTAAAGAATCAGATTGGAGATAAAGAAAAGCTGGGAGGTAAC
 TTTCTCTGAAGATAAGGAGACCATGGAAGAAAGCTGTAGAAGAAAAGATTGAATGGCTGGAAGCCACCA
 AGATGCTGACATTGAAGACTTCAAAGCTAAGAAGAAGGAACCTGGAAGAAATTGTTCAACCAATTATCAGC
 AAACCTCTATGGAAGTGCAGGCCCTCCCCCAACTGGTGAAGAGGATACAGCAGAAAAAGATGAGTTGTAGA
 CACTGATCTGCTAGTGTGTAATATTGTAAATACTGGACTCAGGAACCTTTTGTAGGAAAAAATTGAAAG
 30 AACTTAAGTCTCGAATGTAATTGGAATCTTCACCTCAGAGTGGAGTTGAACTGCTATAGCCTAAGCGGC
 TGTTTACTGCTTTTTCATTAGCAGTTGCTCACATGTCTTTGGGTGGGGGGGAGAAGAAGAATTGGCCATCT
 TAAAAAGCAGGTAAAAAACCTGGGTAGGGTGTGTGTTTACCTTCAAATGTTCTATTTAACAACCTGGGT
 CATGTGCATCTGGTGTAGGAAGTTTTTCTACCATAAGTGACACCAATAAATGTTTGTATTATTACACTGG
 TCTAATGTTTGTGAGAAGCTTCTAATTAGATCAATTACTTATTTTAGGAAATTTAAGACTAGATACTCGT
 35 GTGTGGGTGAGGGGAGGGAGTATTGGTATGTTGGGATAAGGAAACACTTCTATTTAATGTTCTCCAGGG
 ATTTTTTTTTTTTTTTTTTAACCTCCTGGGCCAAGTGATCCTTCCACCTCAGTCTCCAGCTAATTGA
 GACCACAGGCTTGTACCACCATGCTCGGCTTTTGCAATTAATCTAAGAAAAGGGGAGAGAAGTTAATCCA
 CATCTTTACTCAGGCAAGGGGCATTTACAGTGCCCAAGAGTGGGGTTTTCTTGAACATACTTGGTTTTCC
 TATTTCCCTTATCTTTCTAAACTGCCTTTCTGGTGGCTTTTTTTTAAATTATTACTAATGATGCTTTT
 40 ATAGCTGCTTGGATTCTCTGAGAAATGATGGGGAGTGAGTGATCACTGGTATTAACCTTTATACACTTGA
 TTTTCAATTTGTAATTTAGGATGTAAAGGTATATTGTGAACCTTAGCTGTGTCAGAATCTCCATCCCTGAA
 ATTTCTCATTAGTGGTACTGGGGTGGGATCTTGGATGGTGACATTGAACTACACTAAATCCCTCACTA
 TGAATGGGTGTTAAAGGCAATGGTTTGTGTCAAACTGGTTTAGGATTACTTAGATTGTGTTCTCTGAAG
 45 AAAAGAGTCCAGGTAAATGGTATGATCAATAAAGGACAGGCTGGTGCTAACATAAAATCCAATTTAGTAA
 TCCTAGCACTTTGGGAGGCCAAGGCGGGTGGATCACAAGGTCAAGAGATAGAGACCATCTTTGCCAACAT
 GGTGAACTCCATCTCTACTGAAAATACAAAAATTAGCTGGGCGTGGTAGTGCAAGCTGAAGGCTGAGGC
 AGGAGAATCACTCGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGATCACACCACTGTACTCCAGCCCG
 GCACTCCAGCCTGGCGACAAGAGTGAGACTCCACCTCAAAAAAAAAAAAAAGAATCCAATACTGCCCAAG
 50 GATAGGTATTTTATAGATGGGCAACTGGCTGAAAGGTTAATTCTCTAGGGCTAGTAGAACTGGATCCCAA
 CACCAACTCTTAATTAGACCTAGGCCTCAGCTGCACTGCCCGAAAAGCATTTGGGCAGACCCTGAGCAG
 AATACTGGTCTCAGGCCAAGCCCAATACAGCCATTAAAGATGACCTACAGTGCTGTGTACCCTGGGGCAA
 TAGGGTTAAATGGTAGTTAGCAACTAGGGCTAGTCTTCCCTTACCTCAAAGGCTCTCACTACCGTGGAAC
 ACCTAGTCTGTAACCTCTTCTGAGGAGCTGTTACTGAATATTAAAAAGATAGACTTCAAAAAAAAAAAAAA
 AAAAA

SEQ ID NO:129

>gi|16507237|ref|NP_005338.1| heat shock 70kD protein 5 (glucose-regulated protein, 78kD); BiP; Heat-shock 70kD protein-5 (glucose-regulated protein, 78kD) [Homo sapiens]

MKLSLVAAMLLLLSAARAEEDKKEDVGTVVGIDLGTTYSCVGVFKNGRVEIIANDQGNRITPSYVAFTP
 EGERLIGDAKNQLTSNPENTVFDKRLIGRTWNDPSVQQDIKFLPFKVVEKKTKPYIQVDIGGGQTKTF

APPEISAMVLTKMKETAEAYLGKKVTHAVVTVPAYFNDAQRQATKDAGTIAGLNMRIINEPTAAAIAYG
LDKREGEKNILVFDLGGGTFDVSLLTIDNGVFEVVATNGDTHLGGEDFDQVRMEHF I KLYKKKTGKDVRK
DNRAVQKLRREVEKAKRALSSQHQAIEIESFYEGEDFSETLTRAKFEELNMDLFRSTMKPVQKVLEDS
5 LKXSDIDEIVLVGGSTRIPKIQQLVKEFFNGKEPSRGINPDEAVAYGAAVQAGVLSGDQDTGDLVLLDVC
PLTLGIETVGGVMTKLI PRNTVVP TKKSQIFSTASDNQPTVTIKVYEGERPLTKDNHLLGTFDLTGIPPA
PRGVPQIEVTFEIDVNGILRVTAEDKGTGNKNKITITNDQNRLTPEEIERMVNDAEKFAEEDKKLKERID
TRNELESYAYS LKNQIGDKEKLGGKLSSEDKETMEKAVEEKIEWLESHQDADIEDFKAKKKELEEIVQPI
ISKLYGSAGPPPTGEEDTAEKDEL

10 SEQ ID NO:130

IFNgR1

>G3_2_37_PCR_G3F1 Direction: sense

CTGGCTTTAACTCTGACCCAAAGTAGTATTTGATGGATCACCAACATGTATCAGTAAATATTACAATAATGNATG
TAGTAATATTGATGCAGGCATCAATCCATTCTGAATTCTTAACACCATAGTTCTTTACCTCTACGGTAAAAACAG
15 GGACCTGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTG
GTGTAGGCACTGAGGACGGCCCCAGATCCGCGGTGCCCATCTCAGCCCTGCTCACACCCGTCATGACAAGGGGTA
GGAGAAAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCAGCG
CTGCCC

20 SEQ ID NO:131

>GL3_2.37_A_M13F Direction: sense

CTGGCTTTAACTCTGACCCAAAGAGAATTTGATGGATCACCAACATGATCAGAAATATTACAATAATGATGAGAA
ATATTGATGCAGGCATCAATCCATTCTGAATTCTTAACACCATAGTTCTTTACCTCTACGGTAAAAACAGGGACC
TGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTGGTGT
25 GGCACTGAGGACGGCCCCAGATCCGCGGTGCCCATCTCAGCCCTGCTCACACCCGTCATGACAAGGGGTAGGAGA
AAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCAGCGCTGCC
C

SEQ ID NO:132

30 >GL3_2.37_A_M13R Direction: anti-sense

GGGCAGCGCTGGGCTGGTCCCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCT
TTCTCTACCCCTTGTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGTCCTCAGTGC
CTACACCAACTAATGTTACAATTGAATCCTATAACATGAACCCTATCGTATATTGGGAGTACCAGATCATGCCAC
AGGTCCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTAAAGAATTGAGAATTGAGATGGATTGATGCCTGCATCAATA
35 TTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCTCTTTGGGTGAGAGTTAAAGCCA
G

SEQ ID NO:133

40 >GL3_2.37_B_M13F Direction: anti-sense

GGGCAGCGCTGGGCTGGTCCCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCT
TTCTCTACCCCTTGTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGTCCTCAGTGC
CTACACCAACTAATGTTACAATTGAATCCTATAACATGAACCCTATCGTATATTGGGAGTACCAGATCATGCCAC
AGGTCCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTAAAGAATTGAGAATTGAGATGGATTGATGCCTGCATCAATA
45 TTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCTCTTTGGGTGAGAGTTAAAGCCA
G

SEQ ID NO:134

50 >GL3_2.37_B_M13R Direction: sense

CTGGCTTTAACTCTGACCCAAAGAGAATTTGATGGATCACCAACATGATCAGAAATATTACAATAATGATGAGAA
ATATTGATGCAGGCATCAATCCATTCTGAATTCTTAACACCATAGTTCTTTACCTCTACGGTAAAAACAGGGACC
TGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTGGTGT
GGCACTGAGGACGGCCCCAGATCCGCGGTGCCCATCTCAGCCCTGCTCACACCCGTCATGACAAGGGGTAGGAGA
AAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCAGCGCTGCC
55 C

55 SEQ ID NO:135

>GL3_2.37_C_M13F Direction: anti-sense

GGGCAGCGCTGGGCTGGTCCCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCT
TTCTCTACCCCTTGTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGTCCTCAGTGC
60 CTACACCAACTAATGTTACAATTGAATCCTATAACATGAACCCTATCGTATATTGGGAGTACCAGATCATGCCAC

AGGTCCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTTAAGAATTGAGAAATGGATTGATGCCTGCATCAATA
TTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCTCTTTGGGTCAGAGTTAAAGCCA
G

5 SEQ ID NO:136

>GL3_2.37_C_M13R Direction: sense

CTGGCTTTAACTCTGACCCAAAGAGAATTTGATGGATCACCAACATGATCAGAAATATTACAATAATGATGAGAA
ATATTGATGCAGGCATCAATCCATTCTGAATTCCTAACACCATAGTTCTTTACCTCTACGGTAAAAACAGGGACC
TGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTGGTGTA
10 GGCACGTAGGACGGCCCCAGATCCGCGGTGCCCATCTCAGCCCTGCTCACACCCTGCATGACAAGGGGTAGGAGA
AAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCCAGCGCTGCC
C

SEQ ID NO:137

15 >GL3_2.37_D_M13F Direction: sense

CTGGCTTTAACTCTGACCCAAAGAGAATTTGATGGATCACCAACATGATCAGAAATATTACAATAATGATGAGAA
ATATTGATGCAGGCATCAATCCATTCTGAATTCCTAACACCATAGTTCTTTACCTCTACGGTAAAAACAGGGACC
TGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTGGTGTA
GGCACGTAGGACGGCCCCAGATCCGCGGTGCCCATCTCAGCCCTGCTCACACCCTGCATGACAAGGGGTAGGAGA
20 AAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCCAGCGCTGCC
C

SEQ ID NO:138

25 >GL3_2.37_D_M13R Direction: anti-sense

GGGCAGCGCTGGGCTGGTCCCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCT
TTCTCCTACCCCTTGTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGTCCTCAGTGC
CTACACCAACTAATGTTACAATTGAATCCTATAACATGAACCTATCGTATATTGGGAGTACCAGATCATGCCAC
AGGTCCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTTAAGAATTGAGAAATGGATTGATGCCTGCATCAATA
TTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCTCTTTGGGTCAGAGTTAAAGCCA
30 G

SEQ ID NO:139

>gi|4557879|ref|NM_000416.1| Homo sapiens interferon gamma receptor 1
(IFNGR1), mRNA

35 CCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCTTTCTCCTACCCCTT
GTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGTCCTCAGTGCCTACACCAA
CTAATGTTACAATTGAATCCTATAACATGAACCTATCGTATATTGGGAGTACCAGATCATGCCACAGGT
CCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTTAAGAATTGAGAAATGGATTGATGCCTGCATCAAT
ATTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCTCTTTGGGTCAGAGTTA
40 AAGCCAGGGTTGGACAAAAAGAACTCGCCTATGCAAAGTCAGAAGAATTTGCTGTATGCCGAGATGGAAA
AATTGGACCACCTAAACTGGATATCAGAAAGGAGGAGAAGCAAATCATGATTGACATATTTACCCTTCA
GTTTTTGTAAATGGAGACGAGCAGGAAGTCGATTATGATCCCGAAACTACCTGTTACATTAGGGTGTACA
ATGTGTATGTGAGAATGAACGGAAGTGAGATCCAGTATAAAATACTCACGCAGAAGGAAGATGATTGTGA
CGAGATTCAAGTGCAGTTAGCGATTCCAGTATCCTCACTGAATTCTCAGTACTGTGTTTCAGCAGAAGGA
45 GTCTTACATGTGTGGGGTGTACAACTGAAAAGTCAAAAGAAGTTTGATTACCATTTTCAATAGCAGTA
TAAAAGGTTCTCTTTGGATTCCAGTTGTTGCTGCTTTACTACTCTTTCTAGTGCTTAGCCTGGTATTTCAT
CTGTTTTTATATTAAGAAAATTAATCCATTGAAGGAAAAAGCATAATATTACCCAAGTCCCTTGATCTCT
GTGGTAAGAAGTGCTACTTTAGAGACAAAACCTGAATCAAAATATGTATCACTCATCACGTCATACCAGC
CATTTTCTTTAGAAAAGGAGGTGGTCTGTGAAGAGCCGTTGTCTCCAGCAACAGTTCAGGCATGCATAC
50 CGAAGACAATCCAGGAAAAGTGGAACATACAGAAGAAGTTCTAGTATAACAGAAGTGGTGACTACTGAA
GAAAATATTCTGACGTGGTCCCGGGCAGCCATCTGACTCCAATAGAGAGAGAGAGTTCTTCACCTTTAA
GTAGTAACCAGTCTGAACCTGGCAGCATCGCTTTAACTCGTATCACTCCAGAAATTGTTCTGAGAGTGA
TCACTCCAGAAATGGTTTTGATACTGATTCCAGCTGTCTGGAATCACATAGCTCCTTATCTGACTCAGAA
TTTCCCCCAAATAATAAAGGTGAAATAAAAACAGAAGGACAAGAGCTCATAACCGTAATAAAAGCCCCCA
55 CCTCCTTTGGTTATGATAAACACATGTGCTAGTGGATCTACTTGTGGATGATAGCGGTAAAGAGTCCTT
GATTGGTTATAGACCAACAGAAGATTCCAAAGAATTTTCATGAGATCAGCTAAGTTGCACCAACTTTGAA
GTCTGATTTTCTGGACAGTTTTCTGCTTTAATTTTCATGAAAAGATTATGATCTCAGAAATTGTATCTTA
GTTGGTATCAACCAATGGAGTGACTTAGTGTACATGAAAGCGTAAAGAGGATGTGTGGCATTTCCTT
TTGGCTGTAAAGTACAGACTTTTTTTTTTTTTTAAACAAAAAAGCATTGTAACCTTATGAACCTTTTACA
60 TCCAGATAGGTTACCAGTAACGGAACATATCCAGTACTCCTGGTTCCTAGGTGAGCAGGTGATGCCCCAG

GGACCTTTGTAGCCACTTCACTTTTTTCTTTCTCTGCCTTGGTATAGCATATGTGTTTTGTAAGTTTA
TGCATACAGTAATTTTAAGTAATTTTCTCGAAGCTTTTCAAATTTGGACTTAAAACTTAA
TTCAAATAATAGAATTAATGGAATATGTAAATAGAAACGTGTATATTTTTTATGAAACATTACAGTTAG
AGATTTTTTAAATAAAGAATTTTAAACTC

SEQ ID NO:140

>gi|4557880|ref|NP_000407.1| interferon gamma receptor 1; Immune
interferon, receptor for [Homo sapiens]

MALLFLLPLVMQGVSRAMGTADLGPSSVPTPTNVTIESYNMNPVYWEYQIMPQVPVFTVEVKNYGVKN
SEWIDACINISHHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFVCRDQKIGPPKLDIRKEEKQ
IMIDIFHPSVFNVDGEQEVDDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEIQCQLAIPVSSLN
SQYCVSAEGLVHVWGVTTTEKSKEVCITIFNSSIKGSLWIPVVAALLLFLVLSLVFICFYIKKINPLKEKS
IILPKSLISVRSATLETKPESKYVSLITSYQPFSLKEKEVVCEPLSPATVPGMHTEDNPGKVEHTEELS
SITEVVTTEENIPDVVPGSHLTPIERESSPLSSNQSEPGSIALNSYHSRNCSESDHSRNGFDTDSSCLE
SHSSLSDSEFPNNKGEIKTEGQELITVIKAPTSFGYDKPHVLVDLLVDDSGKESLIGYRPTEDSKEFS

SEQ ID NO:141

Importin a4

>GL2_91_2_M13F Direction: sense

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTTTC
TGCCACTTATTGTTAAGTTGCTGATTGCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTTGTTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACATCAC
AATTGAGAACAACCTGGGTCTGCTCGTGGTGCCAGTCACTATGTTGCCAACTGCTCTGAGGGCTGCTGTTTGAA
CTTTGACTTCTGATGGCTCAGAAGGGGCACAAGAAAGGGCACAACCTCTGAATTCCAATAACCATCTGGTATCT
GTTCAATTACCTTCATCTGTCAAAGTTATGACAGAGCCCCAAACAAGTGTCTTACAAGAAATGTTTATATCTGGA
ATGGGTAATATGAAGGACAACATAAAAGGC

SEQ ID NO:142

>GL2_91_1_M13R Direction: sense

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTTTC
TGCCACTTATTGTTAAGTTGCTGATTGCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTTGTTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACATGCTTCCTTATTTATCTTCTCTTTAGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACATCA
CAATTGAGGAACAACCTGGGTCTGACTCGTGGTGCCAGTCACTATGTTGCCAACTGCATCTGAGGGCTGCTG
TTTGAAACTTTGACTTCCCTGATGGCTCAGAAGGGGCACAAGAAAGGGCNACAAACTCTGGAATCNCAATAAAC
AATCTGTATCTGTTCAATAACCTCCATCCTTGGTGCAAAGGTANCTGAACACGGGAGGCCCCAAACAGGTGGT
CCTACAAGGAAATGGTGAACAAACATGGAAATGGGAATAGGANGGACCACCACATAAAGG

SEQ ID NO:143

>GL2_91_3_M13R Direction: sense

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACGAGGTACTCAACCTGATCTTTTC
TGCCACTTATTGTTAAGTTGCTGATTGCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTTGTTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAACGAGATTTGGGAAGTGTGACAGGACATCA
CAATTGAGGAACAACCTGGGTCTGCTCGTGGTGCCAGTCACTATGTTGCCAACTGCTCTGAGGGCTGCTGTTTTG
AACTTTGACTTCTGATGGCTCAGCAAGGGGCACAAGAAAGGGCACAACCTTCCCTGAAAATCCAATAAACCA
TCTGTAATTCTGGTTACATTTACCTTCCAATTCTTGGTTCAAAGGTATGACAGAAGCCCCAAAACAGGTGTTCT
ACCAAGAAATGTTTACATAATCCTGAATGGGAATANTGACNGGACACACATTAAAGCCGCAAAAACCANACANA
CAAAACCAGAC

SEQ ID NO:144

>GL2_202_1_M13R Direction: anti-sense

CTTTAGTGTCTCATATACCATACAGATATAAACATTCTTGTAGACACTGTTTGGGCTCTGTCTACTTTGACAG
ATGGAGGTAATGAACAGATACAGATGGTTATTGATTACAGAGATTGTGCCCTTTCTTGATGCCCCCTTCTTTGGGGA
AAANCCCCAAACTCCACGGGGAGAGCGTCCNAACAAAGNGTTTCCCCACAAAACAAGCACCACAACGCGGCCG
AAGGACACCGCAGTTCCAACNGGAAAAAGAGGAGAGCCCAACACACGGGAGCATAATATNTGAGGGGGGGGCC

AAGAAAAACACCCGCAACTTAAAANGCGCNTGGGGAAGAGCCATTAGGTGGGNNCAACCGCCCCGGGAAAAAGCCGC
GGAAAAAGGGCCCAANGGAAAAACACCCACCCCANCCCCAANAACACGGGGGGGAGAATGCATCACGGGGCGAG
ATCAATACCAGATTTACCCAAAAAACATTACAACG

5 SEQ ID NO:145

>GL2_202_1_M13F Direction: sense

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGGTTTAAACAAGGTACTCAACCTGATCT
TTTCTGCCACTTATTGTTAAGTTGCTGATTGCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGG
10 CTGATGAATTATCATAGGAATTAATCCAG

SEQ ID NO:146

>GL2_66_F10_G3F1 Direction: N/A

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAANCACCTGAACCACTTGAG
15 AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGGGACTCAACTGATCTTTTC
TGGCACTTATTGGTAAAGTTGCTGATTGGCCAAGGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGA
TGAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGGNACCTGTTGCAGGGTTGACCTGCTGGATAATGT
TTGGGAAGGAAACACACTGGGTTCCCTTAATTTATCTTATCTCTATAGGGAGTGATAAGAGATATATGGGAAAGT
20 TGTTAACAGGACATTACAATTTGATGAACAACCTGGGTCTGATACGTCCNCAGNTGGGCCCACNCGCAACGCAAA
TAAGTTTGGGCCCACAACCAGGGGGGCCACGAAAAGAGGACGCAGCCACGTGGGNTTGGAGAACCATCTTGA
AACANTACCTCNGGAATAGAGCGTCCCAANAGGGGGCGGACCCAAGGAANAAAGGGGGACCAAAGTACCTTGG
AAATCCACACATAAAACCATACTGTAATACTCGTGTGCCACGCTGTTAATACCCANTTACCAACAATCCACTG
GGGTCNACACAGGATNANTTGAAAGCACACGGAAGAGAGCGCCAACAACCAAGNNGGGGTGCNGTTNTGCCAAG
CAACCACANGGGTGCGCTGAAGTAGCAATAACCAGGANAANTGGGGGGGACGAGCAACTTNGTAAAGGGTGAACG
25

SEQ ID NO:147

>GL2_91_1_M13F Direction: anti-sense

CTTTATGTGTCCTCATATACCATACAGATATAAACATTCTTGTTAGACACTGTTTGGGCTCTGTCATACTTGACAG
ATGGAGGTAATGAACAGATACAGATGGTTATTGATTACAGGAGTTGTGCCCTTTCTTGTGCCCTTCTGAGCCATC
30 AGGAAGTCAAAGTTCAAACAGCAGCCCTCAGAGCAGTTGGCAACATAGTGACTGGCACCGACGAGCAGACCCAGG
TTGTTCTCAATTGTGATGTCCTGTACACTTCCCAATCTCTTATCACACCCAAAAGAGAAGATAAAATAAGGAAG
CAGTAGTGGTTCCCTTTCCAACATAACAGCAGGCAANCAGCAACAAGTTCAAGCTGTAATAGATGCTGGATTAATT
CCTATGATAAATTCATCAGCNTTGCTAAGNNGGGACATATTGGAAACACAAAAAGAAGCTGCATATGGGGCAAC
AATCAGGCAAANC
35

SEQ ID NO:148

>GL2_91_2_M13R Direction: anti-sense

CTTTATGTGTCCTCATATACCATACAGATATAAACATTCTTGTTAGACACTGTTTGGGCTCTGTCATACTTGACAG
ATGGAGGTAATGAACAGATACAGATGGTTATTGATTACAGGAGTTGTGCCCTTTCTTGTGCCCTTCTGAGCCATC
40 AGGAAGTCAAAGTTCAAACAGCAGCCCTCAGAGCAGTTGGCAACATAGTGACTGGCACCGACGAGCAGACCCAGG
TTGTTCTCAATTGTGATGTCCTGTACACTTCCCAATCTCTTATCACACCCAAAAGAGAAGATAAAATAAGGAAG
CAGTGTGGTTCCCTTTCCAACATAACAGCAGGCAACCAGCAACAAGTTCAAGCTGTAATAGATGCTGGATTAATTC
CTATGATAAATTCATCAGCTTGCTAAGGGGGACTTTGGAACACAAAAAGAAGCTGCTTGGGCAATCAGCAACTTAA
CAATAAGTGGCAAGAAAAGATCAGGTTGAGTACCTTGACAGCAGAATTGTAAATACCACCGTTCTGTAAATTT
45

SEQ ID NO:149

>GL2_91_3_M13F Direction: anti-sense

CTTTATGTGTCCTCATATACCATACAGATATAAACATTCTTGTTAGACACTGTTTGGGCTCTGTCATACTTGACAG
ATGGAGGTAATGAACAGATACAGATGGTTATTGATTACAGGAGTTGTGCCCTTTCTTGTGCCCTTCTGAGCCATC
50 AGGAAGTCAAAGTTCAAACAGCAGCCCTCAGAGCAGTTGGCAACATAGTGACTGGCACCGACGAGCAGACCCAGG
TTGTTCTCAATTGTGATGTCCTGTACACTTCCCAATCTCTTATCACACCCAAAAGAGAAGATAAAATAAGGAAG
CAGTGTGGTTCCCTTTCCAACATAACAGCAGGCAACCAGCAACAAGTTCAAGCTGTAATAGATGCTGGATTAATTC
CTATGATAAATTCATCAGCTTGCTAAGAGGGGACTTTGGAACACAAAAAGAAGCTGCTTGGGCAATCAGCAAACTT
AACAATAAAGTGGCAGAAAAGATCAGGTTGAGTACCTCGTACAGCAGAATGTAATACCACCGTACTGTTAACT
55 TNTACCTGTGAGTGAACAGATCCTCAAGTGGATCANAGAGGGACCTAGAATGGGTCTTAAAAAAAACAATNTC
TGGATAAATTNNGGGCCGGGAGGACATGAAAAGCAAAGGCAACAATCAAGGACACGGAACGAGAAACCAAGCANA
CACATAGGAAGACCACCCGNTGAGCCAACCCGGGACTATGAGGAGGGGCTGCCCCCATGGANACAGGAGCAGC
GACCCAAGNCCAAAAAAGGGGCGAATACAGTAGAACAAGAGNAGNAACAACACCATACAAGAGAGAANAACACC
GACAGCCA
60

SEQ ID NO:150

>GL2_66_F07_G3F1 Direction: N/A

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTTTC
TGCCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTGTTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACATCAC
AATTGAGAACAACCTGGGTCTGCTCGTCCGGTGCCAGTCACTATGTTGCCAACTGCTCTGAGGGCTGCTGTTTGAA
CTTTGACTTCCTGATGGCTCAGAAGGGGCACAAGAAAGGGCACAACCTCCTGAATCAATAACCATCTGTATCTGTT
CATTACCTCCATCTGTCAAGTATGACAGAGCC

SEQ ID NO:151

>GL2_66_F08_G3F1 Direction: N/A

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTTTC
TACCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTGTTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACATCAC
AATTGAGAACAACCTGGGTCTGCTCGTCCGGTGCCAGTCACTATGTTGCCAACTGCTCTGAGGGCTGCTGTTTGAA
CTTTGACTTCCTGATGGCTCAGAAGGGGCACAAGAAAGGGCACAACCTCCTGAATCAATAACCATCTGTATCTGTT
CATTACCTCCATCTGTCAAGTATGACAGAAGCCCAAACAGCTGTCTACAAGAATGTTTATATCTGTATGGTATAT
TGAAGGACACCATAAAG

SEQ ID NO:152

>GL2_66_F09_G3F1 Direction: N/A

CTATTGTGCTTGCTTCATCACCGGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTG
AGAATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTT
TCTGCCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTG
ATGAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTGGTTGCTGGTTGCCTGCTGTTATGTTGG
AAAGGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACAT
CACAATTGAGAACAACCTGGGTCTGCTCGTCCGGTGCCAGTCACTATGTTGCCAACTGCTCTGANGGCTGCTGTTTG
AAGTTGACTTCCTGATGGCTCAAAGGGGCACAAGAAAGGGCACAACCTCCTGAATCAATAACCATCTGTATCTGT
GTCATTACCTCCATCTGTCAAGTATGACAGAGCCCAAACAGTGTCTACACAGCAATGTTCTATATCTCGTATGGN
GATATGAGGGACACCTNAAAGCCG

SEQ ID NO:153

>gi|4504898|ref|NM_002267.1| Homo sapiens karyopherin alpha 3 (importin
alpha 4) (KPNA3), mRNA

AATTCGTGGTTCCAGAATCGATAGGGCTCCAAGATTCGCCGCCGCCGCCGCCGAGCCGCAGGAGTAGCC
GCCGCCGGAGCCGCGCGCAGCATGGCCGAGAACCCAGCTTGGAGAACCACCGCATCAAGAGCTTCAAGA
ACAAGGGCCGCGATGTGGAACAATGCGAAGACATAGAAATGAAGTGACAGTGGAAGTGCAGGAAAGAACAA
AAGAGATGAACACTTATTGAAAAAGAGAAATGTTCCCAAGAAGAAAGTCTAGAAGATTGAGATGTTGAT
GCTGATTTTAAAGCACAAAATGTAACCCCTAGAGCTATATTGCAGAATGCCACAAGTGATAACCCAGTGG
TCCAATTGAGTGCTGTCCAGGCAGCAAGAAAACCTGTTATCCAGTGACCAGAATCCACCGATTGATGACTT
AATAAAATCTGGGATTTTACCAATTCTAGTCAAATGTCTAGAAAGGGATGATAATCCTTCATTACAGTTT
GAAGCTGCTTGGGCATTAACATAAGCATCAGGAACCTCTGCACAGACTCAAGCTGTTGTGAGTCTA
ATGCAGTACCTCTTTTCTGAGACTTCTTCGTTCCACCATCAGAATGTTTGTGAACAAGCAGTATGGGC
TTTGGGAAACATTATAGGTGATGGTCCTCAATGTAGAGATTATGTCATATCACTGGGAGTTGTCAAACCT
CTTCTGTCTTCATCAGTCCCTCCATCCCATCACCTTCTCTCGGAACGTCACATGGGTCAATTGTCAATC
TCTGCAGGAATAAGGATCCCCACCGCTATGGAGACAGTTCAGGAGATTTTGCCAGCTTTATGTGTCTCT
CATATACCATAACAGATATAAACATTTCTGTAGACACTGTTTGGGCTCTGTCTACTTTGACAGATGGAGGT
AATGAACAGATACAGATGGTTATTGATTCAGGAGTTGTGCCCTTTCTTGTGCCCTTCTGAGCCATCAGG
AAGTCAAAGTTCAAACAGCAGCCCTCAGAGCAGTTGGCAACATAGTACTGGCACCGACGAGCAGCCCA
GGTTGTTCTCAATTGTGATGTCTGTCACTTCCCAAATCTCTTATCACACCCAAAAGAGAAGATAAAT
AAGGAAGCAGTGTGGTTCTTTCCAACATAACAGCAGGCAACCAGCAACAAGTTCAAGCTGTAATAGATG
CTGGATTAATTCCTATGATAATTCATCAGCTTGTCTAAGGGGGACTTTGGAACACAAAAGAAGCTGCTTG
GGCAATCAGCAACTTAACAATAAGTGGCAGAAAAGATCAGGTTGAGTACCTTGTACAGCAGAATGTAATA
CCACCGTTCTGTAATTTACTGTCTAGTGAAAGATTCTCAAGTGGTTCAGGTGGTTCTAGATGGTCTAAAAA
ACATTCTGATAATGGCCGGTGATGAAGCAAGCACAATAGCTGAAATAATAGAGGAATGTGGAGGTTTGGGA
GAAAATTGAAGTTTACAGCAACATGAAAATGAAGACATATATAAATTAGCATTGAAATCATAGATCAG

TATTTCTCTGGTGATGATATTGATGAAGATCCCTGCCTCATTCCTGAAGCAACACAAGGAGGTACCTACA
ATTTTGATCCAACAGCCAACCTTCAAACAAAAGAATTTAATTTTAAATTCAGTTGAGTGCAGCATCTTT
CCCACATTCAATATGAAGCACCACCAGATGGCTACCAAATGATAAGAACAACAGCAACAAAAGGCTCCAA
AACACACATGCCCTCTTTGTTTTGATGCTTCTAAAGAAAGCCATGTCTCAGTCAC'TTGCAGTTGCCAAAA
5 GTCACTATCACATGGACTGTAAATGCATATGCATGATTTCTTAAACTGTTTTAGAACTCTCCTTAACAAT
CTCAACTACCTTATTTTTCCCTGTTCCCTGGTGCCACAGGCTGACAACTGCAGTCTCCAGTTTGAATAA
ATATTCCATAGTGGTGACATGTGAGCTGCCACTGATACTCCTTTGGAAAATGGTGCGCTGTGGATCAAG
ACACTTTGGTATGATGCATATACAAGTTGGAAGACTAAAGAGGTGCAATGTGATCTGAGCCTCCATCATT
10 GTCTCCACAAACATATTTTCATATTCTTTATGTGGAAGAATAGATTTTAAAGTACAAGCCAAATGATTT
TCATTGGTGGAAC TGACACAAAAAAGTAACTTAAAAACAAGAACTTGGTTATTGAATAAACAGATAA
GTTTT

SEQ ID NO:154

>gi|4504899|ref|NP_002258.1| karyopherin alpha 3; importin alpha 4 [Homo
15 sapiens]
MAENPSLENHRIKSFKNKGRDVETMRRHRNEVTVELRKNKRDEHLLKKRNV PQEESLESDVDADFKAQN
VTLEAILQNATSDNPFVQLSAVQAARKLLSSDQNPPIDDLKSGILPILVKCLERDDNPSLQFEAAWALT
NIASGTSAQTOAVVQSNAPLFLRLRLSPHQNVCEQAVWALGNIIGDGPQCRDYVISLGVVKPLLSFISP
20 SIPITFLRNVTWVIVNLCRNKDP PPPMETVQEILPALCVLIYHTDINILVDTVWALS YLTDGGNEQIQMV
IDSGVVFPFLVPLLSHQEVKVQTAALRAVGNIVTGTDEQTQVVLNCDVLSHFPNLLSHPKEKINKEAVWFL
SNITAGNQQQVQAVIDAGLIPMI IHQLAKGDFGTQKEAAWAISNLTISGRKDQVEYLVQQNVIPPF CNLL
SVKDSQVVQVVDGLKNILIMAGDEASTIAEIIIECCGLEKIEVLQQHENEDIYKLAF EIIDQYFSGDDI
DEDPCLIP EATQGGTYNFDPTANLQTKEFNF

25 SEQ ID NO:155

Lysosomal pepstatin-insensitive protease (CLN2)
>GL3_21A_2_M13F Direction: N/A
CCATTTCAATACTATGTGGTCGTTACAATGCTAGAGGTAGTGACAGGGGGCGCAATGCAAGGGAGGAAGGGCGT
TAACATCTGCCACCTACTTCCAGGTGCCAAGCACTGTTATCAACATTATTCAC'TTTATTTCCCCTGGGTGATTAT
30 GAAAGGCCAGGTATTGAGTATTCACACTTNACAGACGAGGAAAAACAAGCGCTCAGGGNAGAATAAGCGTTACTTG
ANCCAGGTCATACAATACGTTACCTAGAGTCCCANTTATTTCTAGGAAACCACAGGAGTTTCCAAAACAGGGGTG
TTTGGTGT'TNAGGAAACAATCNTATGGGGAGATATTTTCCAAGCGCAATTACCACAACATTATAAAGTANGCCT
CCAGGGGGGAAAATCAAACCATTCCACGAAAAGAAAGGGTNGAACAT'TCTGGAGAGCATTGAAGGATCTTTGCG
CAAAGAAATTCCTTGGGAAAAATTTTACCCTGGGCAAGGTATGTTATCAAGAGGGGTGGGTAAAGGGGGGNACC
35 GGGAGAACAAAGCGTTTGAAGCGCA

SEQ ID NO:156

>GL3_21A_4_M13F Direction: N/A
CCATTTCAATACTATGTGGTCGTTACAATGCTAGAGGTAGGCACAGGGGGCGCAATGCAAGGGAGGAAGGGCGTT
40 AACAAATTCCTGGCGCACGCTAACTTTCAGGTGGCCAAGGCCACTGGTTATCAACCAGTTATTCCACGTTTATT
TCCCCTGGGTGGGAATTTACTGGAAAAAGGGGGCCAAGGGGGTTAAATTGGAGTATTACACTTTTATACAGACG
AGGGAAACAGGCCTCAGGGAGATAAGCTTACTTGACCCAAGTCTCTCGTCCTTAGGTCCATATCCAGGGAAACCC
AAAGGGAATTTTCCAAAACCAGG

45 SEQ ID NO:157

>GL3_21A_1_M13F Direction: N/A
CCATTTCAATACTATGTGGTCGTTACAATGCTAGAGGTAGGCACAGGGGGCGCAATGCAAGGGAGGAAGGGCGTT
AACATCTGCCACCTACTTCCAGGTGCCAAGCACTGTTATCAACATTATTCAC'TTTATTTCCCTGGTGATTATGAA
AGGCAGGTATTGATATTACACTTAACAGACGAGGAAACAGCCTCAGGGAGATCAAGCTTACTTGACCCAGTCTC
50 TCTCCTAGTTCCATATCAGAACCAAGATTCAAACAGGTTTGGTTTAGAAAATCTAGGATTTTTCAGCCATACCAA
AATAAAGTAGCCTCAGGGAATCAAACATTACGAAAGAAGGTGACTTCTGAACTGAGTCTTGCAAGAAATCTGG
AAATTAACCTGGCAGTTGTATCAGGGGTGGTAAGGGGACGGAA

>GL3 21A 2 M13R Direction: anti-sense

5

>GL3 21A 3 M13F Direction: N/A

10

>GL3_21A_3_M13R Direction: anti-sense

20

>GL3_21A_4 M13R Direction: anti-sense

2.5

>GL3 21A PCR G3F1 Direction: N/A

35

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>gi|5597012|ref|NM_000391.2| Homo sapiens ceroid-lipofuscinosis, neuronal  
2, late infantile (Jansky-Bielschowsky disease) (CLN2), mRNA
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45

5 ACACGTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCCTCAGGTGACAGTGGGGCCGG
 GTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAGCCCCCTATGTCACCACA
 GTGGGAGGCACATCCTTCCAGGAACCTTCTCATCACAAATGAAATTGTTGACTATATCAGTGGTGGTG
 10 GCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAGGAAGCTGTAACGAAGTTCCTGAGCTCTAGCCC
 CCACCTGCCACCATCCAGTTACTTCAATGCCAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTCTGAT
 GGCTACTGGGTGGTTCAGCAACAGAGTGGCCATTCCATGGGTGTCCGGAACCTCGGCCCTTACTCCAGTGT
 TTGGGGGATCCTATCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAA
 CCCAAGGCTCTACCAGCAGCATGGGGCAGGACTCTTTGATGTAACCCGTGGCTGCCATGAGTCTGTCTG
 15 GATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGCTGGGGAACAC
 CCAACTTCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCTTCTCTATCAGGAGAGATGGCTTGTG
 CCCTGCCCTGAAGCTGGCAGTTTCACTCCCTTATTTCTGCCCTGTTGGAAGCCCTGCTGAACCCCTCACTAT
 TGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAATGCGGTGAGCTTGACTTGACTCCCAACCCCTACC
 ATGCTCCATCATACTCAGGTCTCCCTACTCCTGCCTTAGATTCTCAATAAGATGCTGTAACCTAGCATT
 20 TTTGAATGCCTCTCCCTCCGCATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAG
 ACTCTGTGCACTATTTCACTTGATATTCATTCCCAATTCACTGCAAGGAGACCTCTACTGTCCACCGTTT
 ACTCTTTCCTACCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATGGCC
 TTTCCATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTTCTCTGACTACTCTTGT
 CTTCTCTCTCATCAATTTCTGCTTCTTCTCATGGAATGCTGACCTTCATTGCTCCATTTGTAGATTTTGTG
 25 TCTTCTCAGTTTACTCATTGTCCCTTGAACAAATCACTGACATCTACAACCATTACCATCTCACTAAAT
 AAGACTTTCTATCCAATAATGATTGATACCTCAAATGTAAGATGCGTGATACTCAACATTTTCATCGTCCA
 CCTTCCCAACCCCAACAATTCCATCTCGTTTCTTCTTGGTAAATGATGCTATGCTTTTCCAACCAAGC
 CAGAAACCTGTGTCTCTTTTCAACCCACCTTCAATCAACAAGTCTCAATCAACAAGTCCCTACTGACTG
 CACATCTTAAATATATCTTTATCAGTCCACAAGTCTTCCAATTATATTTCCCAAGTATATCTAGAATT
 ATCCACTTATATCCCACTGCTACTACCTTAGTTTAGGGCTATATTCTCTTGAAGGAGTGTCTTACT
 30 TCCTGCCAATCCCAAGTCATCTTCCAGAGTAAATGCAATCCCATCAGGCCACTTGGATGAAACCCCT
 TCAAGGATTACTGGATAGAATTGAGGCTTTCCCTCCAGCCCCCAATCATAGCTCACAAACCTTCTTGC
 TATTTGTTCTTAAGTAAAAAATCATTTTCTCTCTCTCTCCCAACCCCAAGGAACTCTCACTCTTGTCT
 CAAGCTGTTCCGTCCTTACCACCCCTGATAACAATGCCAGGTAAATTTCCAGAATTCTTGCAAGACTC
 AGTTCAGAAGTCACCTTCTTTCGTGAATGTTTTGATTCCCTGAGGCTACTTTATTTTGGTATGGCTGAAA
 35 AATCCTAGATTTTCTAAACAAAACCTGTTTGAATCTTGGTCTGATATGGACTAGGAGAGACTGGGT
 AAGTAAGCTTATCTCCCTGAGGCTGTTTCTCTGTTAAGTGTGAATATCAATACCTGCTTTTCATAA
 TCACCAGGGAATAAAGTGAATAATGTTGATAACAGTGTGTCACCTGGAAGTAGGTGGCAGATGTTAA
 CGCCCTTCTCTCTTGCATGCGCCCCCTGTGCCTACCTCTAGCATTGTAACGACCACATAGTATTGAAA
 TGGCCAGTTTACTTGTCTGCCTTCTTCCAGACCGTTGGTGCCTAGAGGACTAGAATCGTGTCTTATT
 40 TAACCTTGTGTTCCAGGTCTAGCTCAGGAGTTGGCAAATAAGAATTAAATGTCTGCTACACCGAAACA
 AA

SEQ ID NO:164

40 >gi|5729770|ref|NP_000382.3| ceroid-lipofuscinosis, neuronal 2, late
 infantile (Jansky-Bielschowsky disease) [Homo sapiens]
 MGLQACLLGLFALILSGKCSYSPEPDQRRRLPPGWVSLGRADPEEELSLTFALRQONVERLSELVQAVSD
 PSSPQYGYKLTLENVADLVRPSPLTLHTVQKWLAAAGAKCHSVITQDFLTCLWSIRQAEILLPGAEFHH
 YVGGPTETHVVRSPHPYQLPQALAPHVDFVGGHLRFPPTSSLRQRPEPQVTGTVLHLGVTPSVIRKRYN
 45 LTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFNGNFAHQASVARVVGQGRGRAGIEASLDVQYL
 MSAGANISTWVYSSPGRHEGQEPFLQWLMLLSNESALPHVHTVSYGDDSDLSAYIQRVNTELMKAAAR
 GLTLLFASGDSGAGCWSVSGRHQFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPS
 YQEEAVTKFLSSSPHLPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPVWSGTSASTPVFGGILSLINE
 50 HRILSGRPPLGLFNPRLYQOHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPNFPALLKTL
 LNP

SEQ ID NO:165

Novel protein disulfide isomerase
 Novel (disulfide isomerase-like)
 55 CGGACCAACACAGTATTGAGTCAACTGTGACCTTAAGATCAGAGGAACGTCAATACTGCCACAAGGCCACCTTTC
 CAGAACTCGTGGGCAGGTAAACTATGCTTTGGATGTGCTTCTTTCACCAAAATCACTCAACTCAGGAGCCACAA
 ATAGTCCAGCAATTTCACTTCCCTCAACGCTATTTTAGTCTCAAAGGAAACCATGTAAATTTTCATCAAGAGAAGG
 TCAAAGGGGATATATCGCCACTGAAATGTTTACACAGTGACCATGAGTTACACATTTACTTAGAGAACTTAAC
 TTAATAAAGAATCTGTAGAGTGTGTTGGCTTGGGAAACACACACAAAGAAGATACCTCAGCGTTAGTATGTTT
 60 TGCTTTCTGAACAGCCACCACTGGGAACCCAGTGGCCTCTGTGGGACTGAACTCCTAAACGAGGTTGCGGGAGC
 TGGGCAGGAGAGGTGACCTCAACTGTGTTCTTAAAGTTCGTCTTTCGCTTGGCTCAGGACAAAGCGGTGTAACG

AGTCAAAGTCTCTGCCTCCACTGTGCTCACTGACTTTCTTCCCTCCTCGGAAAAGCAATAACGTGGGGTAGCCTC
GT

SEQ ID NO:166

5 Microtubule-associated protein 4 (MAP4)

>GL1_19_HIGH_3_G3F1 Direction: sense

CCACCTCCATTTCTGGAGGCAGACATACGTTCTTGATGAGAACTACTTCTGTTTCTGGAGGTGGAGTCACATCCT
TGCCAGAGCCATTTCTGTTTCTGATAGTG

SEQ ID NO:167

>GL1_19_HIGH_3_G3R1 Direction: anti-sense

CACTATCAGAAACAGAAATGGCTCTGGGCAAGGATGTGACTCCACCTCCAGAAACAGAAAGTAGTTCTCATCAAGA
ACGTATGTCTGCCCTCCAGAAATGGAGGTGG

SEQ ID NO:168

>GL1_19_LOW_2_G3F1 Direction: sense

CCACCTCCATTTCTGGAGGCAGACATACGTTCTTGATGAGAACTACTTCTGTTTCTGGAGGTGGAGTCANATCCT
TGCCAGAGCCATTTCTGTTTCTGATAGTG

SEQ ID NO:169

>gi|14195631|ref|NM_002375.2| Homo sapiens microtubule-associated protein 4
(MAP4), transcript variant 1, mRNA

TGCGACCGCCTCCCTGCGCCCCGCCCCCTCCGGCTAGCTCGCTGGCTCCCGGCTCCTCCCGACGTCCTCTA

CCTCCTCACGGCTCTTCCCGCGCTCTCCTGGCTCCCTTCTGCCCCAGCTCCGTCTCGGCGGCGGCGGGC

25 AGTTGCAGTGGTGCAGAAATGGCTGACCTCAGTCTTGCAATGATGAGAACTACTTCTGTTTCTGGAGGTGGAGTCACATCCT

GGGAGAGATAAAGCGGGACTTCAATGCCCACACTAGAGGCAGAGGCCCTTTGATGATGTTGTGGGAGAACT

GTTGGAAAAACAGACTATATTCCTCTCCTGGATGTTGATGAGAAAAACCGGGAACCTCAGAGTCAAGAAGA

AACCGTGCTCAGAACTAGCCAGATTGAAGATACTCCATCTTCTAAACCAACACTCCTAGCCAATGGTGG

TCATGGAGTAGAAGGGAGCGATACTACAGGGTCTCCAACCTGAATTCCTTGAAGAGAAAATGGCCTACCAG

30 GAATACCCAAATAGCCAGAACTGGCCAGAAAGATACCAACTTTTGTTCCTTGAAGAGAAAATGGCCTACCAG

CTATCCAGACTGATCCCTTTAAGATGTACCATGATGATGACCTGGCAGATTTGGTCTTTCCCTCCAGTGC

GACAGCTGATACTTCAATATTTGCAGGACAAAATGATCCCTTGAAAGACAGTTACGGTATGTCTCCCTGC

AACACAGCTGTTGTACCTCAGGGGTGGTCTGTGGAAGCCTTAAACTCTCCACACTCAGAGTCTTTGTTT

CCCCAGAGGCTGTTGCAGAACCTCCTCAGCCAACGGCAGTTCCCTTAGAGCTAGCCAAGGAGATAGAAAT

35 GGCATCAGAAAGAGAGGCCACCAGCACAAGCATTGGAAATAATGATGGGACTGAAGACTACTGACATGGCA

CCATCTAAAGAAACAGAGATGGCCCTCGCCAAGGACATGGCACTAGCTACAAAACCGAGGTGGCATTGG

CTAAAGATATGGAATCACCCACCAATTAGATGTGACACTGGCCAAGGACATGCAGCCATCCATGGAATC

AGATATGGCCCTAGTCAAGGACATGGAATACCCACAGAAAAAGAGTGGCCCTGGTTAAGGATGTCAGA

TGGCCACAGAAACAGATGTATCTTCAGCCAAGAATGTGGTACTGCCACAGAAACAGAGGTAGCCCCAG

40 CCAAGGATGTGACACTGTTGAAAGAAACAGAGAGGGCATCTCTATAAAAATGGACTTAGCCCCCTTCCAA

GGACATGGGACCACCCAAAGAAAACAAGAAAGAAACAGAGAGGGCATCTCTATAAAAATGGACTTGGCT

CCTTCCAAAGGACATGGGACCACCCAAAGAAAACAAGATAGTCCAGCCAAGGATTTGGTATTACTCTCAG

AAATAGAGGTGGCACAGGCTAATGACATTATATCATCCACAGAAATATCCTCTGCTGAGAAGGTGGCTTT

45 GTCTCTCAGAAACAGAGGTAGCCCTGGCCAGGGACATGACACTGCCCCCGGAAACCAACGTGATCTTGACC

AAGGATAAAGCACTACCTTTAGAAGCAGAGGTGGCCCCAGTCAAGGACATGGCTCAACTCCAGAAACAG

AAATAGCCCCGGCCAAGGATGTGGCTCCGTCCACAGTAAAAGAGTGGGCTTGTGTAAGGACATGTCTCC

ACTATCAGAAACAGAAATGGCTCTGGGCAAGGATGTGACTCCACCTCCAGAAACAGAAAGTAGTTCTCATC

AAGAACGTATGTCTGCCCTCCAGAAATGGAGGTGGCCCTGACTGAGGATCAGGTCCAGCCCTCAAAACAG

AAGCACCCCTGGCTAAGGATGGGGTTCTGACCCTGGCCAACAATGTGACTCCAGCCAAGATGTTCCACC

50 ACTCTCAGAAACAGAGGCAACACACAGTTCCAATTAAAGACATGGAAATTGCACAAACACAAAAGGAATA

AGTGAGGATTTCCATTTAGAATCTCTGCAGGATGTGGGCGAGTCAGCTGCACCTACTTTTCATGATTTAC

CAGAAACCATCACAGGAACGGGGAAAAAGTGCAGCTTGCCGGCGAGGAGGATTCTGTGTTAGAAAAACT

AGGGGAAAGGAAACCATGCAACAGTCAACCTTCTGAGCTTTCTTCAGAGACCTCAGGAATAGCCAGGCCA

GAAGAAGGAAGGCTGTGGTGAAGTGGGACAGGAAATGACATCACCAACCCACCGAACAAGGAGCTCCAC

55 CAAGCCCAGAGAAGAAAACAAAGCCTTTGGCCACCACTCAACCTGCAAAGACTTCAACATCGAAAGCCAA

AACACAGCCCACTTCTCTCCCTAAGCAGCCAGCTCCCAACCATTTGGTGGGTGAATAAAAAACCCATG

AGCCTTGCTTCAGGCTTAGTGCCAGCTGCCCCACCCAAACGCCCTGCCGTGCTCTGCCAGGCCTTCCA

TCTTACCTTCAAAAGACGTGAAGCCAAAGCCCATTGCAGATGCAAAGGCTCCTGAGAAGCGGGCCTCACC

ATCCAAGCCAGCTTCTGCCCCAGCCTCCAGATCTGGGTCCAAGAGCACTCAGACTGTTGCAAAAACACA

60 ACAGCTGCTGCTGTTGCCCTCACTGGCCCCAAGCAGTAGGAGCCCCCTCCACGCTCCTGCCCAAGAAGCCCA

CTGCCATTAAAGACTGAGGGAAAACTGCAGAAAGTCAAGAAGATGACTGCAAAGTCTGTACCAGCTGACTT
 GAGTCGCCCCAAGAGCACCTCCACCAGTTCCATGAAGAAAACCACCCTCAGTGGGACAGCCCCCGCT
 GCAGGGGTGGTTCCAGCCGAGTCAAGGCCACACCCATGCCCTCCCGGCCCTCCACAACCTCTTCATAG
 5 ACAAGAAGCCACCTCGGCCAAACCCAGCTCCACCACCCCCCGCTCAGCCGCCTGGCCACCAATACTTC
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SEQ ID NO:170

>gi|4505099|ref|NP_002366.1| microtubule-associated protein 4, isoform 1
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SEQ ID NO:171

>gi|14195625|ref|NM_030884.1| Homo sapiens microtubule-associated protein 4
 (MAP4), transcript variant 2, mRNA
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SEQ ID NO:172

>gi|14195626|ref|NP_112146.1| microtubule-associated protein 4, isoform 2
[Homo sapiens]

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SEQ ID NO:173

>gi|14195627|ref|NM_030885.1| Homo sapiens microtubule-associated protein 4
(MAP4), transcript variant 3, mRNA

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30 SEQ ID NO:174

>gi|14195628|ref|NP_112147.1| microtubule-associated protein 4, isoform 3
 [Homo sapiens]

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50 SEQ ID NO:175

>gi|14195629|ref|NM_030983.1| Homo sapiens microtubule-associated protein 4
 (MAP4), transcript variant 4, mRNA

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TCAACTCCCAGAAACAGAAATAGCCCCGGGCAAGGATGTGGCTCCGTCCACAGTAAAGAGTGGGCTTG
15 TTGAAGGACATGTCTCCACTATCAGAAACAGAAATGGCTCTGGGCAAGGATGTGACTCCACCTCCAGAAA
CAGAAGTAGTTCTCATCAAGAACGTATGTCTGCCTCCAGAAATGGAGGTGGCCCTGACTGAGGATCAGGT
CCCAGCCCTCAAAACAGAAGCACCCCTGGCTAAGGATGGGGTTCTGACCTGGCCAACAATGTGACTCCA
GCCAAAGATGTTCCACCACCTCTCAGAAACAGAGGCAACACCAGTTCCAATTAAGACATGGAATTTGCAC
AAACACAAAAAGGAATAAGTGAGGATTCCCATTAGAAATCTCTGCAGGATGTGGGGCAGTCAGCTGCACC
TACTTTCATGATTTTACCAGAAACCATCACAGGAACGGGGAAAAAGTGCAGCTTGCCGGCCGAGGAGGAT
20 TCTGTGTTAGAAAACTAGGGGAAAGGAAACCATGCAACAGTCAACCTTCTGAGCTTTCTTCAGAGACCT
CAGGAATAGCCAGGCCAGGAAGAAGGAGGCTGTGGTGGTGGGACAGGAAATGACATCACCACCCACCC
GAACAAGGAGCTCCACCAAGCCCAGAGAAGAAAAAAGCCCTTTGGCCACCACCTCAACCTGCAGAGACT
TCAACATCGAAAGCCAAAACACAGCCCACTTCTCTCCCTAAGCAGCCAGCTCCCACCACCATTTGGTGGGT
TGAATAAAAAACCCATGAGCCTTGCTTCAGGCTTAGTGCCAGCTGCCCCACCCAAACGCCCTGCCGTGCG
25 CTCTGCCAGGCCCTTCCATCTTACCTTCAAAGACGTGAAGCCAAAGCCCATTCAGATGCAAGGCTCCT
GAGAAGCGGGCCTCACCATCCAAGCCAGCTTCTGCCCCAGCCTCCAGATCTGGGTCCAAGAGCACTCAGA
CTGTTGCAAAAACCACAACAGCTGCTGCTGTTGCCTCAACTGGCCCCAAGCAGTAGGAGCCCCCTCCACGCT
CCTGCCCAAGAAGCCCACTGCCATTAAGACTGAGGGAAAACTGCAGAAAGTCAAGAAGATGACTGCAAG
TCTGTACCAGCTGACTTGAGTCGCCCCAAGAGCACCTCCACCAGTTCATGAAGAAAACCACTCTCA
30 GTGGGACAGCCCCGCTGCAGGGGTGGTTCCAGCCGAGTCAAGGCCACACCCATGCCCTCCCGGCCCTC
CACAACCTCCTTTCATAGACAAGAAGCCCACCTCGGCCAAACCCAGCTCCACCACCCCGGCTCAGCCGC
CTGGCCACCAATACTTCTGCTCCTGATCTGAAGAATGTCCGCTCCAAGGTTGGCTCCACGGAACATCA
AGCATCAGCCTGGAGGAGGCCGGGTTAGATTGAGAACAGAAAGTGGACATCTCTAAGGTCTCTCCAA
GTGTGGGTCTAAGGCTAATCAAGCACAAGCCTGGTGGAGGAGATGTCAAGATTGAAAGTCAGAAGTTG
35 AAC'TTCAAGGAGAAGGCCCAGGCCAAGGTGGGATCCCTCGATAATGTGGGCCACCTACCTGCAGGAGGTG
CTGTGAAGACTGAGGGCGGTGGCAGCGAGGCTCCTCTGTGTCCGGGTCCCCCTGCTGGGGAGGAGCCGGC
CATCTCTGAGGCAGCGCTGAAGCTGGCGCCCCCACTTCAGCCAGTGGCCTCAATGGCCACCCACCCCTG
TCAGGGGGTGGTGACCAAAGGGAGGCCAGCCTTGGACAGCCAGATCCAGGAGACAAATTGAGACCTAC
AGGCTGACGTTCCGGGCAAATAGCCAGGGCCCGCACCGACCGGGGCCGACATTGTCTCCCGCCCCC
40 ACTTCCC'TGGCGGCCCAACTCGGGCTCCCGGGTCTTGGCCCCCTTTCCCGGGCTGTCCACTAGACCAG
TGAGCGCTTGGGCGCCGTGCTGGGCGAGCCCGCTAGGCTCGCCTTCCCTCCTGCTTTGCGTGCCCGGGCA
GCAGCAGCCCTGCCCCACACCTCCTCTCACTCCCCAGCCTGGGCCCATCTCCCTGCTTTGGTCTTGCCCC
ATCACTGCGCCACTGCTCCGTGGAGGAGGTTGGGAGGGGTTGGGGTGGTTGAGGCTAAGTTGGGATCTA
GGAGAGGAGAACCAGATTCTATCCTCATCTTTTTTGGTTC'TTTGGTCCAAACCCAAAAGAACTGACAT
45 GCCCTCCCTTCTCCCTGGATCTACCTGGAGGGAAGAGTGGAGGTGGATTCCGAGTGGTGACAGGACGCTG
ACCGTGGAGCTTAAGCCACTGCCCTCTCCCTCTGGTCCCAAAATGGGCGCCCCCCCCCTCCCCATGCAGGT
GGTGTCCGGGCCCTTCTTGCTGCCCTGCCCAAGTTGGGGGTCACTGCTGCCCTGTCCCCATGCTTAACATA
CCCGCCTAGCTGCTGTACATTTTCTTGTCTTGTCTTTTATTTTCTTAATAACCTAAAACTGGCA
AAATAGTTCTGCAGGTTGAAGCCATGTCTACATGAAAGTCCCTCAGTAAGTGTAGAGGGAACAGGGCGGA
50 GATATCCTTATGCCACCCCGCTGGAGGATGTGGGCAGCTTAGGGCCCTGGAGGCGGTGCGGCAGGGAAG
AGGGGTGCAGAGGCTGTGGCTGGTGGCCGGTCAGGCACACAAGGGGCCCTTGGAGCGTGGACTGGTTGG
TTTTGCCATTTTGTGTGTGTATGCTGCTTTCTTTCTAACCAGAGGCTGGTTTGGCATCTCTGTCC
CATTCCTGGGATCTGGTGGTCAGCCCTAGGATAAAAAAGCCAGGGCTGGAGAACAAGAAAGGGCCAGGAG
55 ATGAATTC

SEQ ID NO:176

>gi|14195630|ref|NP_112245.1| microtubule-associated protein 4, isoform 4
[Homo sapiens]

60 MADLSLADALTEPSPDIEGEIKRDFIATLEAEAFDDVVGETVGKTDYIPLLDVDEKTNSESKKKPCSET
SQIEDTPSSKPTLLANGGHGVEGSDTTGSPTEFLEEKMAQYEPNSQNPEDTNFCFQPEQVVDPIQTD
FKMYHDDDLADLVFPSSATADTSIFAGQNDPLKDSYVPLELAKEIEMASEERPPAQALEIMMGLKTTDMA

PSKETEMALAKDMALATKTEVALAKDMESPTKLDVTLAKDMQPSMESDMALVKDMELPTEKEVALVKDVR
 WPTETDVSSAKNVVLPTEETEVAAPKDVTLKETERASPIKMDLAPSKDMGPPKENKKETERASPIKMDLA
 PSKDMGPPKENKIVPAKDLVLLSEIEVAQANDIISSTEISSAEKVALSSETEVALARDMTLPPETNVILT
 KDKALPLEAEVAPVKDMAQLPETEIAPAKDVAPSTVKEVGLLKDMSPLESETEMALGKDVTPPPETEVVLI
 5 KNVCLPPEMEVALTEDQVPALKTEAPLAKDGVLTLANNVTPAKDVPPLSETEATPVP IKDMEIAQTQKGI
 SEDSHLESLODVGGQSAAPTFMISPETITGTGKKCSLPAEEDSVLEKLGKPCNSQPSELSSSETSGIARP
 EEGRPVVSGTGNIDITPPNKELPPSPEKKTPLATTQPAKTSTSKAKTQPTSLPKQAPPTTIGGLNKKPM
 SLASGLVPAAPPKRPASARPSILPSKDVVKPIADAKAPEKRASPSKPASAPASRSGSKSTQTVAKTT
 10 TAAAVASTGPPSRPSTLLPKPTAIKTEGKPAEVKMTAKSVPADLSRPKSTSTSSMKKTTTSLSGTAPA
 AGVVPSPRVKATPMPSPRPSTPFIDKKPTSAKPSSTTPRLSRLATNTSAPDLKNVRSKVGSTENIKHPGG
 GRVQIQNKVVDISKVSSKCGSKANIKHKPGGGDVKIESQKLNFKKAQAKVGSLDNVGHLPAGGAVKTEG
 GGSEAPLCPGPPPAGEEPAISEAAPEAGAPTSASGLNGHPTLSGGGDQREAQTLDSQIQETN

SEQ ID NO:177

NEDD5

>GL3_21C_2_M13F Direction: sense

CTCATAAGACGAAGCTTCACAAAAGATGTCTAAGCAACAGCCAACTCAGTTTATAAATCCAGAAACACCTTGGCT
 ATGTTGGATTTGCAAACCTCCCCAGAATCAAGTTCACCGAAAATCAGTGAAAAAGGTTTATGAGTTCACACTGA
 TAGGTGNGTCGGTGAATCAGGTCTAGGACAACATCGACTCTCATAAACNAGCCTATTCTAACTGATCTGTACCC
 20 AGAAAGAGTCATACCTGAGTAGCAGGTAATAAACATTGAAAGGAAGTGTCCAGATTGAGGCTTCAAACCTGTT
 GACAATTGAAGAGCGAGGGGTCAATG

SEQ ID NO:178

>GL3_21C_2_M13R Direction: anti-sense

CTTGACCCCTCGCTCTTCAATTTCAACATGTTGAAGCCTCAAATCCTGGGACAGGTTCTTTCAATTTTTCTTGC
 TGCGTCCAGGTATGACTCGTTTCTGGGTACAGATCAGTTAGGAATAGGCTGNTTATGAGAGTCGATATTTCTTAG
 ACCTGATTACCGACCACCATCAGTTGTGAACCTCATAAACCTTTTTTCACTGATTTTTCGGTGAACCTTGATTGGG
 GAGGTTTGCNAATTNCCACATAGCCCGGTGTTNTCTGGATTTATAAAGCTGAGTTGGCTGTTGCTATACGGACCT
 30 CTATATTTGTGAAGCTTCTGCTTATGAG

SEQ ID NO:179

>GL3_21C_3_M13F Direction: anti-sense

CTTGANCCCTCGCTCTTCAATTTCAACAGTTGAAGCCTCAAATCCTGGACAGTTCTTTCAATTTTTCTGCTGCTCC
 AGGTATGACTCTTTCTGGGTACAGATCAGTTAGGAATAGGCTGTTTATGAGAGTCGATTTTCTTAGACCTGATTCT
 35 ACCGACCACCATCAGTGTGAACCTCAAACCTTTTTTCACTGATTTTTCGGTGAACCTTGATTGGGGAGGTTTGCAA
 TCCAACATAGCCAGGTGTTTCTGGATTTATAAAGCTGAGTTGGCTGTTGCTTAGACATCTTTTGTGAAGCTTCGTC
 TTATGAG

SEQ ID NO:180

>GL3_21C_3_M13R Direction: sense

CTCATAAGACGAAGCTTCACAAAAGATGTCTAAGCAACAGCCAACTCAGTTTATAAATCCAGAAACACCTGGCTA
 TGTGGATTGCAAACCTCCCCAATCAAGTTCACCGAAAATCAGTGAAAAAGGTTTGTAGTTACACTGATGGT
 GGTGCGGTGAATCAGGTCTAGGAAAATCGACTCTCATAAACAGCCTATTCTTAAGTATCTGTACCCAGAAAGAGT
 45 CATACTGGAGCAGCAGAAAAAATTGAAAGAACTGTCCAGATTGAGGCTTCAACTGTTGAAATTGAAGAGCGAGG
 GGTCAAG

SEQ ID NO:181

>GL3_21C_PCR_G3F1 Direction: sense

CTCATAAGACGAAGCTTCACAAAAGATGTCTAAGCAACAGCCAACTCAGTTTATAAATCCAGAAACACCTGGCTA
 50 TGTGGATTGCAAACCTCCCCAATCAAGTTCACCGAAAATCAGTGAAAAAGGTTTGTAGTTACACTGATGGT
 CGGTGAATCAGGTCTAGGAAAATCGACTCTCATAAACAGCCTATTCTTAAGTATCTGTACCCAGAAAGAGTCATA
 CCTGAGCAGCAGAAAAAATTGAAAGAACTGTCCAGATTGAGGCTTCAACTGTTGAAATTGAAGAGCGAGGGGTCA
 AG

SEQ ID NO:182

>GL3_21K_PCR_G3F1 Direction: sense

CTCATAAGACGAAGCTTCACAAAAGATGTCTAAGCAACAGCCAACTCAGTTTATAAATCCAGAAACACCTGGCTA
 TGTGGATTGCAAACCTCCCCAATCAAGTTCACCGAAAATCAGTGAAAAAGGTTTGTAGTTACACTGATGGT
 GGTGCGGTGAATCAGGTCTAGGAAAATCGACTCTCATAAACAGCCTATTCTTAAGTATCTGTACCCAGAAAGAGT

CATACCTGGAGCAGCAGAAAAAATTGAAAGAACTGTCCAGATTGAGGCTTCAACTGTTGAAATTGAAGAGCGAGG
GGTCAAG

SEQ ID NO:183

5 >gi|4758157|ref|NM_004404.1| Homo sapiens neural precursor cell expressed,
developmentally down-regulated 5 (NEDD5), mRNA
CCCAGCTCGGTGCTGCCGCCATCTTCTTGGAGGACAGGAGGAGAGGCGAAGGCTCCCCCTCCCCGTGATC
GCTCCGCACTCCCGCCACCACCTGCCCTCCCGCGACCGCTCTCTCCTCCTCAGTGGGCACCTTGTCTCCT
10 TCTAACAAACGGCCTTCCCCCACTCCAGTTACCCACCGCAAGGCGAAGATTTCTCATTACCTGTTCCACT
CTTATAAGCATAAGAAAACCGAGCTCATAAGACGAAGCTTCACAAAAGATGTCTAAGCAACAGCCAATC
AGTTTATAAATCCAGAAACACCTGGCTATGTTGGATTGCAAACTCCCAATCAAGTTCACCGAAAATC
AGTGAAAAAGGTTTTTGAGTTTCACTGATGGTGGTGAATCAGGTCTAGGAAAAATCGACTCTCATA
AACAGCCTATTCTTAAC TGATCTGTACCCAGAAAGAGTCATACCTGGAGCAGCAGAAAAAATTGAAAGAA
15 CTGTCCAGATTGAGGCTTCAACTGTTGAAATTGAAGAGCGAGGGGTCAAGCTACGCCTGACAGTGGTAGA
TACCCCTGGCTATGGTGACGCTATCAACTGCAGAGATTGTTTTAAGACAATTATCTCCTATATTGATGAG
CAATTTGAGAGGTACCTGCATGACGAGAGCGGCTTGAACAGGCGGCACATCATTGATAATAGGGTGCATT
GTTGCTTTTACTTTTATTTACCTTTTGGACATGGACTTAAGCCCTTAGATGTGGCGTTTATGAAGGCAAT
ACACAACAAGGTGAATATTGTGCCTGTCAATTGCAAAAGCTGACACTCTCACCCCTGAAGGAACGGGAGCGG
20 CTGAAGAAAAGGATTCTGGATGAAATTGAAGAACATAACATCAAAATCTATCACTTACCTGATGCAGAAT
CAGATGAAGATGAAGATTTTAAAGAGCAGACTAGACTTCTCAAGGCTAGCATCCCATTTCTCTGTGGTTGG
ATCCAATCAGTTGATTGAAGCCAAAGGAAAGAGGTGAGAGCCGCTTACCCCTGGGGTGTGTGGAA
GTGGAGAACCAGAGCACAATGACTTTCTGAAGCTGAGAACCATGCTCATCACCCACATGCAGGATCTCC
AGGAGGTGACCCAGGACCTTCATTATGAAAACCTCCGTTCTGAGAGACTCAAGAGAGGCGGCAGGAAAGT
25 GGAGAATGAGGACATGAATAAAGACCAGATCTTGCTGGAAAAAGAAGCTGAGCTCCGCCGCATGCAAGAG
ATGATTGCAAGGATGCAGGCGCAGATGCAGATGCAGATGCAGGCGGGGATGGCGATGGCGGGGCTCTCG
GGCACCACGTGTAAGGTGATGTGCACATATCAAGAAGTCAGAGAAAACACTTTCCTGGATAAAAAAGAAA
ACATTTCCAGATGCATGATCCAGCTGTGTGTTTTCAATCCTTGGGAGGGTGCCATCCACATTTTAACAGTA
CCTGTGCCCTGAGAATTTAATTTTTAAAGACTTTGATGTGTTTTGTATGAAGTACTTTTAACGTATGTA
30 TTTTATTGCTGTGTACACTGTGTTTTGTGAGGTGAATGTCTTCTTTCTTCTCCCTAACCACTAA
TGTTAGAATTGATTTCCAAGAAATCGGCATGTATACTTAATCACTGAATTTCTTTGATTTAACTGACTTAA
AACTGACTAACCATTTGATGAGCACTCCTGATTTTTATCTAGAACATTCAGATTTACCATAATGTTCTCTTA
GTGGTAGAGGTGTGTGCCTAGTGATGTAGAAAGATACACTGACTTGGTGCAAGGCCATCTGCTTACCACA
TCACACCACCTGGAGATCTTTGCTTCTTGTCTTTATGTTGTACACAACACCTAAAACAGTTTTGCTG
35 CTATAATTTCTATACTGTTGATTCGTCTGCGATTTTATCTGTTAACCAAATAAAACATAATAGAATTTCT
AATGAGATATATCTTTATACTTAAACAGCTTTTTTTAGAGGTGAGTTTTAAAGAAGTCTCTTAATTCTGAT
GCTAGGTTGTTTTTAAACCACCTATGCAAGAACTCACCACAAGCCACCTTTTGTAGTGTCTTCCACTAA
TACTGGTTATCTCTGTGCTACAGAGAAAATCAAAGCAGTCATAAGCTCCAGTTTTCCGTATTGCAAATAAG
ACTCTTACCTACAAAATGAGATTCAGTGAATAATTTGGTTTTTACTCAACCAAATTAATAATTTTTTT
40 AAGGAAAATTAGCAGTTGGTCTATTGAGAAATCAAAACCTTTTTATATTTTATCTGCACTTTAGTGATTT
TCTGTCACTGTAGGTATAGAAGATCTGCCTCCCTGTGGAAATTGGGGTCTGTTGGTGGGCTTGCCCTG
AAGCCTGGCTTGGGTGAAAAGTGTTCGCCCTTAAGGCCTTGGTGCCCTGAACCTCTGATGCCTACCGG
GTTCTCCTGATTTGAGTTTCTTTAAATACTCCCTTTTTGAGTAATTTCTGATGGGAGGAAAGTAGCAG
TCATCATCTTTTTGTGTGAGGCTGTCTCATTTATTTTAGCCATTGTCGTTTCATTCAATTTTGTGTAAT
45 ATAAACCGTGTGTCAATGTCAAAGTGAAAGACATTTCAAATCTGTAGCATAGGCTAGTGGGCAGGTCCGCA
CAGTCGAAGCCACACCTGGTCTGTTTTCTGTGCACTGTAGCCTTAGTGTCACCTTTCTTCTTGTGTCTCC
TTATGGTACACTCCAGCGGTTGCCTTTTTATCATTTCTACTGAAGTTGGGAAATTCAACCCAGAAATT
GACAGATGAAAGGAGACAATGGTTGTGTAGGGAGATGGAGAAATGCTTAATCTGAGGATGAGACAGGGT
TTTTTCAATTTTTGTGGGGCTAGAAAAAACAATAAATGAGGCAGTTAAATAATAATAGTTAATGAAGGTG
50 TGCTACAGAAAATAATCTGGTGTCTTGTCTAACTTTGCCCTTCACTGTTGCTTAATTGTGAACAGCCAAA
AGCTATATGTTATGGCTTATTGTGTGAAGGTAACATAAGAGTGGTGTTCATGACTTCAGAGTACATCCA
TGCGGAGTCCATTATTTGAGTTTGACATTTAATAACTTTGCTGGAAAATCTGTAAAAAAGAAAAACAAGT
TTGCTAGTGACTAAGCCCCGCATATGTGAGTGAAAGTACTTCAGGCACGCTGCCTCCTGGTAACAGCTAT
GCAGGGAGGGAGGACCCACACTGCTACACTTCTGATCCCCCTTTGGTTTTTACTACCCAAATCTAAATAGAT
ACTTTTGATAATAGATAACTGCTCTTTTACTAAGACATAGTCTCTACCTATAGAAATGTATTTTGAAAC
55 ACTTATTTTACACAGCAATTTTGTATCCATTTAAACTAACCTTTTATCAATAAAGCACTATTGTTTAGAT
ATT

SEQ ID NO:184

60 >gi|4758158|ref|NP_004395.1| neural precursor cell expressed,
developmentally down-regulated 5 [Homo sapiens]
MSKQQPTQFINPETPGYVGFANLPNQVHRKSVKKGFEFTLMVVGESGLGKSTLINSFLFLTDLYPERVIPG

AAEKIERTVQIEASTVEIEERGVLRLTVVDTPGYGDAINCRDCFKTIISYIDEQFERYLHDESGLNRRH
IIDNRVHCCFYFISFPFGLKPLDVAFMKAIHNKNVIVPIAKADTLTLKERERLKKRILDEIBSHNIKI
YHLPDAESDEDEDFKEQTRLLKASIPFSVVGSNQLIEAKGKKVRGRLYPWGVVEVENPEHNDFLKLR TML
ITHMQDLQEVTDQLHYENFRSERLKRGGRKVENEDMNKDQILLEKEAELRRMQEMIARMQAQMOMQMQGG
5 DGDGGALGHHV

SEQ ID NO:185

Novel (breast cancer antigen; tyrosine/serine/threonine kinase)

>G3_3_29_PCR_G3F1 Direction: N/A

10 CAGGGGGTGCTGAAGGCCCTCGAAGTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACAT
CCTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCGCAGCAACCTCAGCATGATAAGCCATGGGCAGCG
GCAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGNTTCTGCCGTGGCTCAGCCCCGAGGTCTCCAGC
AGAATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCC
ATGTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGG
15 ATACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACA
GCCTGACCACCAGCACCCC

SEQ ID NO:186

>GL3_1.36_A2_M13F Direction: N/A

20 CAGGGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
GTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
25 ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACAGC
CTGACC

SEQ ID NO:187

>GL3_1.36_A2_M13R Direction: anti-sense

30 CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGATGGGGGTGACAGGACGAAGCAATTCGGGCCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAGAGAGAGGTTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGNACACCATGGGGCA
AGGAACCATGGCCTGNTGGCAGACGGGCTGTCGGAGCCAACCTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
TTCCGAAGNGGGGTAGTTTCTCTCATTTCAAANGAGGGGAGAGAAANTGGCATCCGGGTTGCGCTGAAGGCAT
35 GCTCCACAAGTGGTGGAAGTGGGGGGAGAAGGTTTCGTTGGTAGGGGTGGGAGGGCGAGTCACCGTAGGNGGGCC
GGGGGGTGCTG

SEQ ID NO:188

>GL3_1.36_B2_M13F Direction: N/A

40 CAGGGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
GTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
45 ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGNCAGC
CTGACCAACAG

SEQ ID NO:189

>GL3_1.36_B2_M13R Direction: anti-sense

50 CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGATGGGGGTGACAGGACGAAGCAATTCGGGCCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAGAGAGAGGTTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGACGGGCTGTCGGAGCCAACCTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
TTCCGAAGCGGGGTAGTTTCTCTCATTTCAAANGAGGGGAGAGAAAGCTG

SEQ ID NO:190

>GL3_1.36_B3_M13F Direction: anti-sense

60 CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGATGGGGGTGACAGGACGAAGCAATTCGGGCCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAGAGAGAGGTTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA

AGGAACCATGGCCTGGTGGCAGACGGGCTGTCTGGAGCCAACTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
TTCGGAAGCGGGGTAGTTTCTCTCATTCAAAGAGGGGAGAGAAAGCTGGCATCCGGGTTCGCTGAAGGCACT
GCTCCACAAAGTGGTGGAAAGTGGGGGAGAAAGTTTCGGTGGTAGGGGTGGGAGGGCGAGTCAACCGTNGGAGGGCC
GGGGGGTGTGGTGGTCANGCTGTCACTCAGGCCAGAGTTGGNCACTGATCGCGAANGGCTCATGGTCAGNTCCT
5 CANCAGGGATGGTGTGGTATCCAACAGGCAGGGCACTGTGCCGTTTTCAGTTTCTCTNAGCAGCATCTGGGTGGCA
GGCATATCCTTAAAGGGGACATGGCCGTTGGCCACTCACAGGCCTGT

SEQ ID NO:191

>GL3_1.36_B3_M13R Direction: sense

10 CAGGGGGTGTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTTCGCGAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACGGCCAAACGGCCAT
15 GTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
ACCAGACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACAGC
CTGACCACCAG

SEQ ID NO:192

>GL3_1.36_B4_M13F Direction: anti-sense

20 CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGTATGGGGGTGACAGGACGAAGCAATTCGGGCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAAGAGAGAGGTGGGTGACAGATCCTGTNGCTCTGGGTCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGANNAGCTGTATAGCCAAACNCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
25 TTCGGAAGCGGGGTAGTTTCTCTCATTCAAAGAGGGGAGAGAAAGCTGGCATCCGGGTTTCGCTGAAGGCAC
GCTCCACAAAGTGGTGGAAAGTGGGGGAGAAAGGTTTCGGTGGTAGGGGTGGGAGGGCGAGTCAACGTTGGAGGGCC
GGGGGGTGTGGTGGTCAGGCTGTCACTCANGCCAGAGTTGGCCACTGACCGCGAAGGGCTCATGGTCAGTTTCCT
CANCAGGGATGGTGTGGTA

SEQ ID NO:193

>GL3_1.36_B4_M13R Direction: sense

30 CAGGGGGTGTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTTCGCGAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACGGCCAAACGGCCAT
35 GTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
ACCAGACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACAGC
CTGACCACCAGCACCCCCC

SEQ ID NO:194

>GL3_10.04_PCR_G3F1 Direction: N/A

40 CAGGGGGTGTGAAGGCCCTCGACTACGTCACCCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTTCGCGAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACGGCCAAACGGNCAT
45 GTCCCTTTAAGGATATGCCTGCCACCCATATGCTGCTAGAGAACTGAACGGCACAGTGCCCTG

SEQ ID NO:195

>GL3_3.29_A_M13F Direction: N/A

50 CAGGGGGTGTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTTCGCGAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACGGCCAAACGGCCAT
GTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
55 ACCAGACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACAGC
CTGACCACCAGCACCCC

SEQ ID NO:196

>GL3_3.29_A_M13R Direction: anti-sense

60 CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGTATGGGGGTGACAGGACGAAGCAATTCGGGCAAAGCCTCTGAGGCAC

GTCGCTTGATCTGGGGGAGAAGAGAGAGGTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGACGGGCTGTCTGGAGCCAACCTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
TTCGGAAGCGGGGTAGTTTCTCTCATTCAAAAAGGAGGGGAGAGAAAGCTGGCATCCGGGTTGCGCTGAAGGCACT
GCTCCACAAAGTGGTGGAAAGTGGGGGAGAAGGTTCCGGTGGTAGGGGTGGGAGGGCGAGTCACCGTTGGAGGGCC
5 GGGGGGTGCTGGTGGTCAGGCTGTCACTCAGGCCAGAGTTGGCCACTGAGCGCGAAGGGCTCATGGTCAGCTCCT
CAGCAGGGATGGTGGTATCCAACAGGCAGGGCACTGTGCCGTTTCACTTTCTCTAGCAGCATCTGGGTGGCAG
GCATATCCTTAAAGGGGACATGGCCGTTGGCCAGTTCACAGGCTGTGATTCCCACACT

SEQ ID NO:197

10 >GL3_3.29_B_M13F Direction: N/A
CAGGGGGTGTGTAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGTTTGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
15 GTCCCCTTTAAGGATATGCCTGCCGCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACCTCTGGCCTGAGTGACAGC
CTGACCACCAGCACCC

SEQ ID NO:198

20 >GL3_3.29_B_M13R Direction: anti-sense
CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGTATGGGGGTGACAGGACGAAGCAATTCCGGGCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAGAGAGAGGTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGACGGGCTGTCTGGAGCCAACCTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
25 TTCGGAAGCGGGGTAGTTTCTCTCATTCAAAAAGGAGGGGAGAGAAAGCTGGCATCCGGGTTGCGCTGAAGGCACT
GCTCCACAAAGTGGTGGAAAGTGGGGGAGAAGGTTCCGGTGGTA

SEQ ID NO:199

30 >GL3_3.29_C_M13F Direction: N/A
CAGGGGGTGTGTAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGTTTGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
GTCCCCTTTAAGGATATGCCTGCCACCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCCTGCCTGTTGGAT
35 ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACCTCTGGCCTGAGTGACAGC
CTGACCACCAGCACCC

SEQ ID NO:200

40 >GL3_3.29_C_M13R Direction: anti-sense
CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGTATGGGGGTGACAGGACGAAGCAATTCCGGGCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAGAGAGAGGTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGACGGGCTGTCTGGAGCCAACCTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
45 TTCGGAAGCGGGGTAGTTTCTCTCATTTCAAAGGAGGGGAGAGAAAGCTGGCATCCGGGTTGCGCTGAAGGCACT
GCTCCACAAAGTGGTGGAAAGTGGGGGAGAAGGTTCCGGTGGTAGGGGTGGGAGGGCGAGTCACCGTTGGAGGGCC
GGGGGGTGTGCTGGTGGTCAGGCTGTCACTCAGGCCAGAGTTGGCCACTGAGCGCGAAGGGCTCATGGTTCAGCTCCT
CAGCAGGGATGGTGGTATCCAACAGGCAGGGCACTGTGCCGTTCA

SEQ ID NO:201

50 >GL3_3.29_D_M13F Direction: N/A
CAGGGGGTGTGTAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAANCCAGNCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGTTTGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCNAGTGGTCCANGANN

SEQ ID NO:202

55 >gi|20559344|ref|XM_044379.3| Homo sapiens similar to serologically defined
breast cancer antigen NY-BR-96 (LOC92335), mRNA
GCGGCGCGCAGTAAACTGAGGAGGCGGAGCCAAGACGGTCCGGGCTGCTTGCTAACTCCAGGAACAGG
TTTAAGTTTTTGAAGTGAAGTAGGCCTACACAGTAGGAACCTCATGTCAATTTCTTGTAAGTAAACCAGAG
60 CGAATCAGGCGGTGGTCTCGGAAAAGTTCATTGTTGAGGGCTTAAGAGATTTGGAACATTTGGAGAGC

AGCCTCCGGGTGACACTCGGAGAAAAACCAATGATGCGAGCTCAGAGTCAATAGCATCCTTCTCTAAACA
GGAGGTGATGAGTAGCTTTCTGCCAGAGGGAGGGTGTACGAGCTGCTCACTGTGATAGGCAAAGGATTT
GAGGACCTGATGACTGTGAATCTAGCAAGGTACAAACCAACAGGAGAGTACGTGACTGTACGGAGGATTA
ACCTAGAAGCTTGTTCGAATGAGATGGTAACATTCTTGAGGGCGAGCTGCATGTCTCAAACCTCTTCAA
5 CCATCCCAATATCGTGCCATATCGAGCCACTTTTTATTGCAGACAATGAGCTGTGGGTTGTACATCATTC
ATGGCATAAGGTTCTGCAAAAGATCTCATCTGTACACACTTCATGGATGGCATGAATGAGCTGGCGATTG
CTTACATCCTGCGAGGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGT
CAAAGCCAGCCACATCCTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGGCGAGCAACCTCAGC
ATGATAAGCCATGGGCAGCGGCAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGT
10 GGCTCAGCCCCGAGGTCTCCAGCAGAATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGG
AATCACAGCCTGTGAACCTGGCCACGGCCATGTCCCTTTAAGGATATGCTGCCACCCAGATGCTGCTA
GAGAAACTGAACCGGCACAGTGGCCTGCTGTGGATACCAGCACCATCCCCGCTGAGGAGCTGACCATGA
GCCCTTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACAGCCTGACCACCAGCACCCCCGGCCCTCAA
CGGTGACTCGCCCTCCACCCCTACCACCGAACCTTCTCCCCCACTTCCACCCTTTGTGGAGCAGTGC
15 CTTACAGCGCAACCCGATGCCAGGCCAGTGCCAGCACCTCTGAACCACTCTTCTTCAAGCAGATCA
AGCGACGTGCCCTCAGAGGCTTTGCCCGAATTGCTTCGTCTGTACCCCCATACCAATTTTGAGGGCAG
CCAGTCTCAGGACCACAGTGGAAATCTTTGGCCTGGTAACAACTGGAAGAGCTGGAGGTGGACGATTGG
GAGTTCTGAGCCTCTGCAAACTGTGCGCATCTCCAGCCAGGGATGCAGAGGCCACCCAGAGGCCCTTCC
TGAGGGCCCGCCACATTCCCGCCCTCTGGGCAGATTGGGTAGAAAGGACATTCTTCCAGGAAAGTTGAC
20 TGCTGACTGATTGGGAAAGAAAATCCTGGAGAGACACTTCACTGCTCCAAGGCTTTTGAGACACAAGGGA
ATCTCAACAACCAGGGATCAGGAGGGTCCAAAGCCGACATTCCAGTCTGTGAGCTCAGGTGACCTCTCT
CCGCAGAAGAGAGATGCTGCTCTGGCCCTGGGAGCTGAATTCCAAGCCAGGGTTTGGCTCCTTAAACCC
GAGGACCGCCACCTCTTCCAGTGCTTGCAGCAGCCTCATTCTATTAACTTTGCTCTCAGATGCCCTCA
GATGCTATAGGTGAGTGAAGGGCAAGTAGTAAGCTGCCTGCCTCCCTTCCCTCAGACCTCTCCCTCATA
25 ATTCCAGAGAAGGGCATTCTGCTCTTTTAAAGCACAGACTAAGGCTGGAACAGTCCATCCTTATCCCTCT
TCTGGCTTGGGCCCCTGACACCTAAGTCTTTCCACGGTTTATGTGTGTGCTCATTCTTTCCACCAAG
AATCCATCTTAGCGCTCCTGCCAGCTGCCCTGGTGTCTTCTCAAGGGCCATCAGTGTCTTGCCTAGCT
TGAGGGCTTAAGTCTTATGCTGTGTTAGTTTCGTTGTCAGAA

SEQ ID NO:203

>gi|14770985|ref|XP_044379.1| similar to serologically defined breast
cancer antigen NY-BR-96 [Homo sapiens]
MSFLVSKPERIRRVWSEKFIVEGLRDLELFGEQPPGDTRRKTNDASSESIASFSKQEVMSFLPEGGCYE
LLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEMVTFLOGLHVSCLFNHPNIVPYRATFIAD
35 NELWVVTSMAYGSAKDLICTHFMGDMNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILISVDGKVV
LSGLRSNLSMISHGQRQVRVHDFPKYSVKVLPWLSPEVLQONLQGYDAKSDIYSVGITACELANGHVFPK
DMPATQMLLEKLNQTVPCLLDSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPSHYPYHRTFSP
HFHHFVEQCLQRNPDPARPSASTLLNHSFFKQIKRRASEALPELLRPVTPITNFEQSQSDHSGIFGLVTN
LBELEVDWDF

SEQ ID NO:204

Novel (chromosome 1)

>GL2_46A_B12_G3F1 Direction: sense

ATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
45 TACCACCTGTTACTTTGACAACTCTAGCTTCAGGGCTACCAGGACCATTTGCAAACTTACACCCACAGAAAAC
CAAAGTCTCCAGAGGCATAAGCTCCAATCCCCCAGAGAGCTCGCACTAGCATTCTTCTCCCTTCTAGTAGTACT
TTTATGGGGGGGAGTTATTTCTTCCCCACAAAAGTGAGCGGCGACAATAAAAACAATGTTTCCCACAAAAGAGTTT
CCCCGGTTCTTCTCCCAAAATTTNGGGGGGGCCCCGTTTNTCCCCCGGGCGACGGGGGCGGGNGGGCCCCGCC
50 TGAATACCGCCCAAGATAGGNCGCCGAAAAAGAGCCAAACCCNNGAAAGAGAGATTTTATATAGAGGAAGCA
AAAACGAAANGANAGCGTTTCTTTTCTTCCNGCCAACAACATGGGGGGCCCCCGTTTATAAATAGAGTT
TTTGTCTTTTAAACAATCGACTTTTCTTCCCCCGTGTATTTAAAAAAGAAGGAAGGGTATTTTATATNTT
GGGGGNGCGTGTATTATATAAATTATTTAGTGGGTGCGGGGANGGAAAGAGNGAAGCTGTTTATCCCATCAAAA
TATTATTGTG

SEQ ID NO:205

>GL2-30-CON-TOPO Direction: sense

ATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
45 TACCACCTGTTACTTTGACAACTCTAGCTTCAGGGCTACCAGGACCATTTGCAAACTTACACCCACAGAAAAC
CAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTGG

TTTCCAGGAAAATCATCTCATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTTCAGCCATTATT
CTAGTTGTATGGAGTCATTCAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACCT
TTGCTAATTTTTCCATAAAATTGAAAGCCTT

5 SEQ ID NO:206

>GL2_46A_B07_G3F1 Direction: N/A

ATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTTGACAACCTCTAGCTTCAGGGGGCTACCAGGACCATTGCAAACTTACACCCACAGAAAA
CTCAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTT
10 GGTTCAGGAAAATCATCTCATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTTCAGCCATT
TTCTAGTTGTATGGAGTCATTCAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACCT
ACCTTTGCTAATTTTTTC

SEQ ID NO:207

15 >GL2_46A_B08_G3F1 Direction: sense

ATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTTGACAACCTCTAGCTTCAGGGGGCTACCAGGACCATTGCAAACTTACACCCACAGAAAAC
CAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTTGG
20 TTTCAGGAAAATCATCTCATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTTCAGCCATT

SEQ ID NO:208

>GL2_46A_B10_G3F1 Direction: sense

ATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTTGACAACCTCTAGCTTCAGGGGGCTACCAGGACCATTGCAAACTTACACCCACAGAAAAC
25 TCAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTTG
GTTTCAGGAAAATCATCTCATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTTCAGCCATTAT
TCTAGTTGTATGGAGTCATTCAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACCT
TTTGCTAATTTTTCCATAAAATTGAAAGCCTT

30 SEQ ID NO:209

>GL2_46A_B11_G3F1 Direction: N/A

AATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAG
CTACCACCTGTTACTTTTGACAACCTCTAGCTTCAGGGCTACAGGACATTGCAAACTTACACCCACAGAAAAC
AAGTCTCCAGAAGCATAAGCTCCAACCCCCAGANAGCTCCAAGATTCTTCTCCTTCTAGTAGTACTTTTTGGTTTC
35 CAGGAAAATCATCTCATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTTCAGCATTATCTAGT
TGTATGTGAGTCCTTCCAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACNTTGGT
AATTTTTCCCTAAATTGAAAGCCTTCCGCAGAAACCAGCACAGTGGTTAGATAGATAAA

SEQ ID NO:210

40 Clone 30 -Novel (Chromosome 1)>

ATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTTGACAACCTCTAGCTTCAGGGGGCTACCAGGACCATTGCAAACTTACACCCACAGAAAAC
CAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTTGG
TTTCAGGAAAATCATCTCATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTTCAGCCATTATT
45 CTAGTTGTATGGAGTCATTCAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACCT
TTGCTAATTTTTCCATAAAATTGAAAGCCTT

SEQ ID NO:211

Novel (chromosome 3; h40)

50 >GL2_46B_C03_G3F1 Direction: N/A

GCGTCGCTCGGCGTTAGCCAAGGCCCGGGCGGCCACCCCTCCGGGGGCACTAGGTCTGGGGCCGAGTGCCCCC
CCATAGGCACACAGAGNGAAGCGCCAATGGGCCTGGGTTTTTTTTAAATTTCCCGGGCGGGGCGNAACCCCGG
AACACAACGGGCAAACCTGTACAATTTTTGTGGGGANCAACAACCGGGACACAANTTTTTGGGGNAATGGCGCCA
CAAAAAAANAACCAACGACGCGACGAAAGCGCGTGGTGTGTGTCNGAATACTTTTTATAAAACCACCAATGG
55 GCGCCTCTCGCTTGTGCGCGCCCCCTTCTCCCCAANGGGGGGGCGCGCTGTTTTTCCCCAACACGGGCGTGGGG
CCCCAAAAAATTTGTGGGCGCCCCAAGAAAAAATTTTAAATAAACAGAGGCGGCCCCCACAACACAGGCGGT
TNTGGGGGAACAGGAAACCAACACAACGACAACACGGCGCTGGCGGCAACAAGCAAACACGGGAGCAAACAAAAC
ACGGGCGGAAAGAAACCAACGCGGCAACGACTTTTTATAACAAACACTTTTGTGGGGCGCAAACAGCACACAC
ACAACCAAAATGGGCGCCCCCCCCNCCGAGGGGGCCCAAAAGGNCGAAGAGAAAAAACACCCCCCCCCAAAA
60 AGAGAGCGCCCGCAAAACAACCAAAAAAAGGGGAGGAGTTTGGAGAGCAGGGCGAGANGTTTTTTTTATATTA

AAACACGGGCNACGAAAACATCATTTTATAAATAGGGCAGGCCAAAAACACGATTTATAATATTTCAACAGAAAA
CAGGGNTGGCCTCTGGGGGTTTGGTGTGTGTGCTTCCNACCGGTGGTGCGCGTGTTCCTCCTGGTGNGGAA
AAAAGACACCTGTTTTATAAAAGAGGAGNGTATTNCCNCCTTTTTGTGGGTGCGAAAAACAGACGNGAGGCGGGA
NGATNTATCCCACTCTTTTGGTGGTGCAACAAGTGTTTTATATAGNATACCTG

5

SEQ ID NO:212

>GL2_46B_C01_G3F1 Direction: N/A

GCGTTGCTCGGCGTTAGCCAAGGGCCCGGGCGGCCACCCCTCCGGGGGCACTAGGTCTGGGGCCGCGAGTGCCCA
GNCACAGAGCAGCGTTTATCTGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGGC
TCANGGGTTCAGGCGAATGCAAATAAGCACGTGAAAAGGAAGAAGACGATAATGAAAAGCCGCAGAAACCAGCAC
AGTGGTTAGAT

10

SEQ ID NO:213

>GL2_46B_C02_G3F1 Direction: sense

CAAGCCGGTGACGCGTTGTCTAGTGTCTGGGTCTGCGGGCGTTGCTTCGGCGTTAGCCAAGCCGGGCGGCGCCA
CCCTCCGGGGGGGGGGCCACTAGGTCTGGGGCCGCGAGTGCCAGCACAGAGCAGCGTTTATCGGGACGAAGAAT
GAATTGGAAAGAATTGGAGCAAAAAGAGGTTGATAACAGCGGCCCTCAGGGGTTTCAGGCAATGCAAATAAGCAGTG
AAAAGGAAGAAGACGATAATGAAAAGCCGCAGAAACCAGCACAGTGGTTAGATAGATAAAGCGGGCGCTCGACTA
GTCTGAGGTCTGATA

15

20

SEQ ID NO:214

>GL2_46B_C04_G3F1 Direction: N/A

GCGTGCTCGGCGTTAGCCAATGCCCCGGGCGGCGCCACCCCTCCGGGGGCACTAGGTCTTGGGGCCGCGAGTGCCAGC
ACAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCTGGCCTCA
GGGGGTTTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGAC

25

SEQ ID NO:215

>GL2_46B_C05_G3F1 Direction: sense

GCGTCGCTCGGCGTTAGCCAAGGCCCGGGCGGCGCCACCCCTCCGGGGGCACTAGGTCTGGGGCCGCGAGTGCCAG
CACAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGCTCAG
GGGTTTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGACGATAATGAAAAG

30

SEQ ID NO:216

>GL2_46B_C06_G3F1 Direction: sense

GCGTCGCTCGGCGTTAGCCAAGGCCCGGGCGGCGCCACCCCTCCGGGGGCACTAGGTCTGGGGCCGCGAGTGCCAG
CACAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGCCTCA
GGGGTTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGACGATAATGAAAAG

35

SEQ ID NO:217

>GL2_95_1_M13R Direction: anti-sense

CTTTTCATTATCGTCTTCTCTCTTTTCACTGCTTATTTGCATTGCCTGAACCCCTGAGGCCGCTGTAATCAACCTC
TTTTTGCTCCAATTCTTTCATTTCATCTTCGTCCCGATAAACGCTGCTCTGTGCTGGGCACTGCGGCCCCAGACC
TAGTGCCCCCGGAGGGTGGCGCGCCCGGGCCTCGGCTAACGCCGAGCGACGC

40

SEQ ID NO:218

Clone 95 -Novel (Chromosome 3/ H41)>

GCGTCGCTCGGCGTTAGCCAAGGCCCGGGCGGCGCCACCCCTCCGGGGGCACTAGGTCTGGGGCCGCGAGTGCCAG
CACAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGCCTCA
GGGGTTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGACGATAATGAAAAG

45

50

SEQ ID NO:219

Novel (chromosome 17)

>GL2_147_1_M13F Direction: anti-sense

CTTGCCATTCCACTCCAGCCTGGGCAACGAGAGCGAAACTCTGTCTCAAAAAGAAAAGAAAAGGAAAAGAAAACC
ACCTCCCAACAGGTTAAATAAATAATTAACATTTTGGTATGTACCCTTCAGACATTTTCCTATGCATCACATCA
ATAAATATATGATAGGATATTTTACATTTGATGTATCCTGAAGATTAATTCAACAAATGTTTATGTAGTAGGCTT
GTTGTAGGTGCTGGGAATTCAGCAGTGAACAAAACAAAGTCTCTGCCTCATGGAGCTCATATTATAGTAGGGAAG
ACTGTCAATAAGCAATATACACATTGACTAAATGATAGATAATGCCAGTAATGTGGCAAGTTTATGGAAAAT
AAATCAGGATAAAAAGGATAAGAGTGATATGGGGATTCTCTTAGTTAGGGTAGATAAGGAAGGCCTCTTAGCTAAG

55

SEO ID NO:220

SEO ID NO:221

SEO ID NO:222

SEO ID NO:223

50 SEO ID NO:224

56

SEQ ID NO:225

>GL2_147_1_M13R Direction: sense

CTGCTTCTCTTCTAGGATAGTTTCCCTCTAGAAATCCATGTTGCTCCTTCTCTCATTAGATGATCAGATATTTAT
GTGCCTCCTTAGCTAAGAGGCCTTCCCTTATCTACCCTAACTAAGAGAATCCCCATATCACTCTTATCCTTTTATC
5 CTGATTTATTTTTCCATAAACTTGCCACATTACTGGGCATTATCTATCATTTAGTAATGTGTATATTGCTTATT
GACAGTCTTCCCTACTATAATATGAGCTCCATGAGGCAGAGACTTTGTTTTGTTCACTGCTGAATTCCCAGCACC
TACAACAAGCCTACTCACTAAACATTTGTTGAATTAATCTTCAGGATACATCAAATGTAAAATATCCTATCATAT
ATTTATTGATGTGATGCATAGGAAAATGTCTGGAAGGGTACATACCAAATGTAAATTATTTATTTAACCTGGTG
10 GGAGGTGGTTTTTCTTTCTTTTCTTTNCTTATTGAGACAGAGTTTCGCTCTCGTTGCCCCGGCTGGAAGTGGAA
TGGCAAGCCGGCAGGAACCCAAGACAACAAGGAGGTTAAGATCAGAATAAAAGACGGGGACCGCATCCAGAAAC

SEQ ID NO:226

>GL2_147_4_M13R Direction: anti-sense

CTTGCCATTCCACTCCAGCCTGGGCAACGAGAGCGAAACTCTGGTCTCAAAAAGAAAGGAAAAGGAAAGAAAAC
15 CACCTCCCACCAGGGTTAAATAAATAATTAACATTTTGGTATGTACCCTTCCAGGACATTTTCTTATGCATCACA
TCAATAAATATATGATAGGATATTTTACATTTGATGTATCCTGAAGATTAATTCAACAAATGTTTAGTGAGTAGG
CNTGTTAGTAGGTGCTGGGAATTGAGCAGTGAACAAAACAAAGTCTCTGCCTCATGGAGCTCATATTATAGTAGG
GAAGACTGTCAATAAGCAATATACACATTACTAAATGATAGATAATGCCAGTAATGTGGCAAGTTTTATGGAAA
AATNAATCAGGATAAAAGGATAAGAGTGATATGGGGATTCTNCTTAGATTAGGGTAGATAAAGGAANGCCTCTTA
20 GNCINAAGAGGCCACATAAACAATAATCAATTCCTTGGGAAAATCCAANCTGNCTAAACGTAGACAGGGACAAGCA
ANAGGCGGACGG

SEQ ID NO:227

Clone 147 - Novel (Chromosome 17)>

CTGCTTCTCTTCTAGGATAGTTTCCCTCTAGAAATCCATGTTGCTCCTTCTCTCATTAAATGATCAGATATTTAT
GTGCCTCCTTAGCTAAGAGGCCTTCCCTTATCTACCCTAACTAAGAGAATCCCCATATCACTCTTATCCTTTTATC
25 CTGATTTATTTTTCCATAAACTTGCCACATTACTGGGCATTATCTATCATTTAGTAATGTGTATATTGCTTATT
GACAGTCTTCCCTACTATAATATGAGCTCCATGAGGCAGAGACTTTGTTTTGTTCACTGCTGAATTCCCAGCACC
TACAACAAGCCTACTCACTAAACATTTGTTGAATTAATCTTCAGGATACATCAAATGTAAAATATCCTATCATAT
30 ATTTATTGATGTGATGCATAGGAAAATGTCTGGAAGGGTACATACCAAATGTAAATTATTTATTTAACCTGGTG
GGAGGTGGTTTTTCTTTCTTTTCTTTTCTTTTGGAGACAGAGTTTCGCTCTCGTTGCCCAGGCTGGAGTGGAAAT
GGCAAG

SEQ ID NO:228

Novel (chromosome 8)

>GL1_41_2_G3F1 Direction: sense

GCTTGCAAAGGAGAGGCTGTGACTACCAAGGTCGTGTCAACAACCTGAATGGCTGAAATACCCAAACTTGCCCATG
CAAATGGGCTTGGGTCTCTCCTGGCAGCCGCCCTTTGAAGGCTCTAGACTTATCTGTGAACCTCTTTTTTTGAGAGG
40 GTCTTTCCAAGTAGTGTTTATTCTTTGACTCTCCTCATACCTTTTTTTGCCAGAGAGTGAGAGTGAGAAGGGAGG
GCTAATGCCTGAGCTCCTGCCCTTTCTATGCAGTGAGGGTCAAGATCCTCAGCTAGTGTGTTGAGGGAAGTGGTGT
AACCTGGGTCTCTCATTTTCTACCATCCAAGTTGCC

SEQ ID NO:229

>GL1_41_2_G3R1 Direction: anti-sense

GGCAACTTGGATGGTAGAAAATGAGAGACCCAGGTTACACCAGGTTCCCTCAAACACTAGCTGAGGATCTTGACC
CTCACTGCNTAGAAAAGGGCAGGAGCTCAGGCATTAGCCCTCCCTTCTCACTCTCACTCTCTGGCAAAAAGGTAT
45 GAGGAGAGTCAAAGAATAAACCAGTAGTTGGAAAGACCTCTCAAAAAGGAGTTACAGATAAGTCTAGAGCCT
TCAAAGGCGGCTGCCAGGAGAGACCCAAGCCCATTTGCATGGGCAAGTTTGGGTATTTAGCCATTAGTTGTTG
50 ACACGACTTGGTAGTCACAGCCTCTCCTTTGCAAGC

SEQ ID NO:230

>GL1_41_3_G3F1 Direction: sense

GCTTGCAAAGGAGAGGCTGTGACTACCAAGTCGTGTCAACAACCTGAATGGCTGAAATACCCAAACTTGCCCATGC
AAATGGGCTTGGGTCTCTCCTGGCAGCCGCCCTTTGAAGGCTCTAGACTTATCTGTGAACCTCTTTTTTTGAGAGGG
55 TCTTTCCAAGTAGTGTTTATTCTTTGACTCTCCTCATACCTTTTTTTGCCAGAGAGTGAGAGTGAGAAGGGAGGG
CTAATGCCTGAGCTCCTGCCCTTTCTATGCAGTGAGGGTCAAGATCCTCAGCTAGTGTGTTGAGGGAAGTGGTGT
GCCTGGGTCTCTCATTTTCTACCATCCAAGTTGCC

SEQ ID NO:231

>GL1_41_3_G3R1 Direction: N/A

GGCAACTTGGATGGTAGAAAAATGAGAGACCCAGGCTACACCAGNTTCCCTCAAACACTAGCTGAGGATCTTGACC
CTCACTGCATAGAAAAGGGCAGGAGCTCAGGCATTAGCCCTCCCTTCTCACTCTCACTCTCTGGCAAAAAGGTAT
5 GAGGAGAGTCAAANAATAAACCACTANTTGGANAGACCCTCTCAANAAAGGAGTTCACAGATAANTNTATAGCCT
TCAAAGGCGGCTGCCAGGAGAGAC

SEQ ID NO:232

Novel (chromosome 8)>

10 GCTTGCAAAGGAGAGGCTGTGACTACCAAGTCGTGTCAACAACTGAATGGCTGAAATACCCAACTTGCCCATGC
AAATGGGCTTGGGTCTCTCCTGGCAGCCGCCCTTTGAAGGCTCTAGACTTATCTGTGAACTCCTTTTTTGGAGAGGG
TCTTTCCAAC TAGTGGTTTATTCTTTGACTCTCCTCATACCTTTTTTGCCAGAGAGTGAGAGTGAGAAGGGAGGG
CTAATGCCTGAGCTCCTGCCCTTTCTATGCAGTGAGGGTCAAGATCCTCAGCTAGTGTGTTGAGGGAAGTGGTGTA
15 ACCTGGGTCTCTCATTTTCTACCATCCAAGTTGCC

SEQ ID NO:233

Novel (chromosome 9)

>GL2-49-5M13R Direction: anti-sense

20 CTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTCGGG
TTGGATGGCTGTGTCCGTCGCCATGTTTGTGTGGTGCCTGGCCCCGTGGTCCCAGTGTCTGGCAGCTTCTGGCTC
CAGCCTCAGCCTGTAGTGGGGTGTACGTGGTAGNGAGTGCGGTAGCTGGGGGCTGCAGTGGGGTAGGTGAGTG
GTAGGAGTGCAGNTAGCATAGAAAGTTANAAAGGTTACTAGTAGAGACTGGTCCCATACTTAGAGATGGGACACCA
TGACCTGATGGNTACNACCCCTGACAGGCCGCAGAAACCAGACACACTGGAGCCACCGACTGACACAACGGGCCNT
GGGNACGGACGTCCAATNGCGTATGANTACCANGACAGTCAGGANCCCCAAATGACCCGGAAGCAGGAAACGGGG
25 CAGAAAAANCAATAGCCAAGGAATAGTCAANGGTCGACANAACCTGNGCAGGGACCAGNAAACCAGAANGACC
AATGCACANTACATAAGAAAGGGGGGGGCACNCCACAAAAGATATGCCGGGCGACGCCAGATAAGATAAGGGACT
AGGGAAGGAGTCCGGGNAANATGTAACGAAAGAGTATCGAACCAATGGAGGNGCGCGGGTACCCGNGCGNAAG
GACAAACAANAAGCAGGCATCCGGACTGGGAACCAATGGGGGGGAAGAAGCAGCGCCCCCATGGGGANAGGGAT
30 GTAAANCCACAACAACACGTGTNAAACG

SEQ ID NO:234

>GL2-49-4M13F Direction: N/A

AATTGAANTTACACTCACTATAGGGCGAATTGGGCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGAAT
ATCTGCAGAAATTCGCCCTTCTCTCGGCATGGACGAGCTGTACAAGGAGGAGGCCGCAAGGCCGGTGGCAGCGGTG
35 GCTCCAAGTGGTGGCCTTGGGGGTTCTTTCGGCTGCAGGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGC
CACAGAAACCTCTAACCTCAGCACTGCACCTCACCACGAACACCCACGCAGGCCCTCAGGCAACCCGGCAACC
TTCCAAACCAACGGAACACCCACACAGGCTGAGGCTGGAGCCAGAAGCCGCGCAGAACATGGGACCACAGGGCCA
GGCACCACACAAACATGGCGACGGACACAGCCAATCCAACCCCGGAAAAACCGATTTCCNCGGNGGGGGAAAA
ACCGCCCCAGTTTTCCACCCCGGGAGAGCGCCCCAAAAGGGGGGGGNACACCCACCCACNCAACCCCAAAGGGGN
40 CGCAGGGGCCAAACAGCAGAAANCCCCGAANTTCCCTTTCGGGGGGAATTTCGCCGCGCCCAAAGGGGAACNAGCA
AGGAAGGCCATTGCCGGTTGCCGGGCCAAGCACCGCCAGGAACAGCGCGCAAGGCGAC

SEQ ID NO:235

>GL2-49-1M13F Direction: sense

45 CTGCAGGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCCCTCTAACCTCAGCACTGCACTC
CACCACGACCACCCACGCAGGCCCTCAGCACCGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCC
AGAAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGA
CTCGGACCTCCGCCAGGCCCCAGCGCACAAACATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:236

>GL2-49-1M13R Direction: anti-sense

50 GCTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTCGG
GTTGGATGGCTGTGTCCGTCGCCATGTTTGTGTGGTGCCTGGCCCTGTGGTCCCAGTGTCTGGCAGCTTCTGGCT
CCAGCCTCAGCCTGTGTGGGGTGTTCGTGGTGGAGTGCGGTGTGAGGGCCTGCGTGGGGTGGTCTGGTGGAGT
55 GCAGTGCTGAGGTTAGAGGGTTTCTGTGGCTGTCCCTCTTAGGTGGGCACCTGCCTGTGGTCTCCCTGCAG

SEQ ID NO:237

>GL2-49-2M13F Direction: sense

60 CTGCAGGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCCCTCTAACCTCAGCACTGCACTC
CACCACGACCACCCACGCAGGCCCTCAGCACCGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCC

AGAAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGA
CTCGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:238

5 >GL2-49-2M13R Direction: N/A
CTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTGGG
TTGGATGGCTGTGTCCGTCGCCATGTTTGTGTGGTGCCTGGCCCTGTGGTCCCATGTTCTGGCAGCTTCTGGCTC
CAGCCTCAGCCTGTGTGGGGTGTTCGTGGTGGAGTGCCTGTGAGGGCCTGCGTGGGGTGGTCTGTGGTGGAGTG
10 CAGTGCTGAGGTTANAGGGTTTCTGTGGCTGTCCCTCTTAGGTGGGCACCTGCCTGTGGTCTCCCTGCAGCCGCA
AAACCCANACACTGGAGCCACCGCTG

SEQ ID NO:239

>GL2-49-4M13R Direction: N/A
15 CTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTGGG
TTGGATGGCTGTGTCCGTCGCCATGTTTGTGTGGTGCCTGGCCCTGTGGTCCCATGTTCTGGCGGCTTCTGGCTC
CAGCCTCAGCCTGTGTGGGGTGTTCGTGGTGGAGTGCCTGTGAGGGCCTGCGTGGGGTGGTCTGTGGTGGAGTG
CAGTGCTGAGGTTAGAGGGTTTCTGTGGCTGTCCCTCTTAGGTGGGCACCTGCCTGTGGTCTCCCTGCAG

SEQ ID NO:240

20 >GL2_72_G07_G3F1 Direction: N/A
CTGCAGGGAGACCCGCAGGCAGGTGCCCACCTAAGGGGGACAGCTACAGAAACCCCTCTAACTCAGCACTGNACTC
CACCACGACACCCACGCAGGCCCTCAGCACCAGCACTCCACCACGAACAACCCACACAGGCTGAGTGCTGGAGCC
AGAAGCTGGCAGAACATGGGACCACAGGGGCCAGGCACCACACAAACATGGCGACGGACACAGGCATNCAAACCG
25 ACTCGGACCTCCGCCAGGNCCTCAGCGCACAAACATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGGCAGCGCA
GAAACCAGCACAGTGGTTAGATATGATTAAAGCGGGCGNGTCGANTAACTGAGGTCTGATACTCACTGACTGTCTG
TAAGGGNGAATTTCGCGGGCGCGTAAATTCATTCGGCCTATAGTGAGTCGTATTACAATTCAGTGGGCGGCGTTT
TACAACGTCTGTGACTGGGAAAAACCTGNGCGTTATCCAACCTAATCTGNGCTTGGAGAATTTCCCTTTTGCAGA
CTGGGCGTAATAACGAAAAAGGNCAGAA

SEQ ID NO:241

30 >GL2_72_G08_G3F1 Direction: sense
CTGCAGGGAGACACAGGCAGGTGCCCACCTAAGAGGGACAGCCACAGAAACCCCTCTAACCTCAGCACTGCACTCC
ACCACGACACCCACGCAGGCCCTCAGCACCAGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCCA
35 GAAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGAC
TCGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:242

>GL2_72_G09_G3F1 Direction: sense
40 CTGCAGGAGACCCGCAGGCAGGTGCCCACCTAAGGGGGACAGCTACAGAAACCCCTCTAACCTCAGCACTGCACTCC
ACCACGAACACCCACGCAGGCCCTCAGCACCAGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCCA
GAAGCTGGCAGAACATGGGACCACAGGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGA
CTCGGACCTCCGCCAGGCCCCCAGCGCACAAACATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:243

45 >GL2_95_2B10_G3F1 Direction: sense
CTGCAGGAGACACAGGCAGGTGCCCACCTAAGAGGGACAGCCACAGAAACCCCTCTAACCTCAGCACTGCACTCCA
CCACGACACCCACGCAGGCCCTCAGCACEGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCCAG
AAGCTGCCAGAACATGGGACCACAGGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGACT
50 CGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:244

>GL2_95_2B11_G3F1 Direction: sense
CCGCAGTGGAGACACAGGCAGGTGCCCACCTAAGAGGGACAGCCACAGAAACCCCTCTAACCTCAGCACTGCACTC
CACCACGACACCCACGCAGGCCCTCAGACCGCACTCCACCACGAAAAACCCACACAGGCGTGAGGCTGGAGCCAG
55 AAGCTGCCAGAACATGGGANACAGGGNCAGGCGACCACACAAACATGGCGACGTGACACAGGCATCCAACCCGA
CATCTGGACTCCGCCAGGGCCCCAGCGCACAAACATACTGGGATCCCCACGAAAAGAGCTGCGTGCTGGGCAGNAG
CGCNAGAAACAGCACAGCTGGTTAGAGTACAGATAAANACGGGCGCGTCGCACGTAAANCTGAAAAAGGTCTGTG
AGTATAATCAACATGTANACTGNTT

SEQ ID NO:245

>GL2-49-5M13F Direction: sense

CTGCAGGGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCCCTCTAACCTCAGCACTGCACT
CCACCACGANACCCCCACGCAGGCCCCCAGCACCGCACTCCACCACGAAACACCCCAACACAGGCTGAGGCTGGA
5 GCCAGAAGCTGGCCAGAACATGGGACCAACGNGCGGNNCCCCAACGNGGGCGGGCCCCAGAACGACCGAAAAGCG
AAACCCCAAAAGAAAGNNGCGCAAATTATGCAGACCAGGAAACCAGATGAAAACAAACCAAAGGCGACCAAATACC
CCAAAANANACCCGCNCAGGAAAGCATACACGCGGGGAAACGCCAGTTCCACCACAGGGGCCCCACAAGGAGGG
GACCCNCCACCACGNGCAGGGGACCGGCCAGCAGACAGCGAGAGCGCCGCGAAGTACCGATTAGGAGGCGGCG
10 AATACCCGACCACCAAAAAGGGGAAACACGAAAGAAAGCTGGGAAACCGCCCCGATTATTAGGACCACGGGAGT
TTGACCGCACGGGGAGACGCCCCCCAAAGGGACACCCCCAGAGGCACAAAAGCAAGAAGACACCCCCCCCCAA
AGAGACCGCTCAAGACCCGAAAGAGGTTGGAGCGGCTTCCTTAACAGAGGAAGCTTAACNCGGCACAGTTNAAAC
GAAGGGCGAGTGGGG

SEQ ID NO:246

>GL2_49_1_M13R Direction: anti-sense

CTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGTGGAGGTCCGAGTCGGG
TTGGATGGCTGATGTCCGCCGCCATGATTTGATAGATGGATGCCTGGACCCTGATGAGTCCCAATGATTCTGGCA
GACATTCTGACATCCAGCACATCAGACCTGATGATGGGGATGNTTCGATGGATG

SEQ ID NO:247

>GL2_49_2_M13R Direction: N/A

CTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTCGGG
TTGGATGGCTGGTTCGCGCAGTGGTGGTGCCTGGCCCTGGGCCTGTCTGGCAGCTTCTGGCTCCAGCCTCAGCCCTG
TGTGGGGCTGGTTCCGNTGGTGGAGTGCGGGTGTGAAGGCCATGCGATGGAGAGTGGATCNAAGGAAGGAGATGC
25 AGAAGCATAGAGAGTTACGAGGGTATCTAGTGGCTGTACCCTCTATAGGTAGGGCACCATTGACACTAGATGGTAC
TNCCTTGACAGAACGCAAGAAACACCAAGAAAACCTGAGAGGCCAACCAGAAATGAC

SEQ ID NO:248

Clone 49 -Novel (Chromosome 9)>

CTGCAGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCCCTCTAACCTCAGCACTGCACTCC
ACCACGACCACCCACGCAGGCCCCCTCAGCACCGCACTCCACCACGAACACCCCAACACAGGCTGAGGCTGGAGCCA
GAAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGAC
TCGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:249

Novel (clone 1/226)

>GL2_1_3_M13F Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGCGCCCTTTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTATATTGGGGGAGG
GAGTAGAAAAGCAAGCCCTATACTGGGCCCTATTAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCT
40 GAGGAAATAAAAGTTGTTTGGAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTG
AAGTGTGAAGGCCCTCATAACCTCCATCTTGCTCAGGACTATAGTCTTGAACCCCTNNGGGCGGAGAAAAGCGC
CAACATTTCAATNCTGCATACATAAGGGAGAAGGAGACAGGACAACGATAAGTGAAAGAGAACAGAACAGCAAG
AAAAGAAGCGGANAACGGCCCCAGACAATAGTAAGGGCGAANGAATGGGCAGAAAGNCTTGCAANCCTNCCCGGGG
GCAATACAATCCCTTGAACACAAGANCCAGGGCANNCCGGGACCACGCAAGAAAACCAAGAAACACAT

SEQ ID NO:250

>GL2_81B_E02_G3F1 Direction: N/A

GCCCGAGCCGGACTGGTCAGGATGATCACCGACGCGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCT
CTTCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGTGAATGAAAGTGGCGCTTTC
50 TCCGGGCCCAGGGTCCAGGACATAGTCTGAGTGCAAGATGGAGGGTATGAGGGGGCTTCACACTTCACTTCATC
CTTTTAACCATTTAAAATACAAAGCGAACTACANCTGGATTTTTTCAAACAAATTTATTTCCTCAGAGTCTTCCT
TAATCCTATGGAACAAGAAGCTGGCACTGAATAGTGGGCCAGTATAGGGGCTTGCGTTTCTANATCCCTTCCCC
CAATATTTAAATATATGACTTTTAAAAAAGGGNGCCGGTTCGCGATCTAGAACTAGTCCGGAGAAA
CCAGACAGTTGGTTAGATAGATAAAGCGGCGCGTCACTANTCTGAGGTCTGATACTCACTGACTGTCTAAGGG
55 CGAATTCGTTTTTAACCTGCAGGACTAGTCCCTTTATGAGGGTTAATTCTGAGCTTGGCGTAATCAT

SEQ ID NO:251

>GL2-96-1M13R Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
60 TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTCTCC

GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCGCTTCACACGTTCACTTCAGTCCCT
TCTACCCATCACAACATACAAGGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCCCTCAGAGTCTTCCTT
AATCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAAT
ATAAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:252

>GL2-96-3M13F Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCGCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGAC

SEQ ID NO:253

>GL2-96-3M13R Direction: N/A

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGGG
AGTAGAAAAGCAAGCCCTATACTGGGCCCTATTAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTG
AGGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTNTGNTATGTTGTGATG

SEQ ID NO:254

>GL2-96-4M13F Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGGGAGTAG
AAAAGCAAGCCCTATACTGGGCCCTATTAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTGAGGAA
ATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAAGTGT
GAAGGCCCTCATACCCTCCATCTTGCTCAGACTATGTCTGGAACCTTGGGGCGGAGAAAGCGCCACTTTTCAT
TCCTGCTTCTTGGGATTGTTGACGGCCACGTAGTGATAGAGAACGACAAGCAAGAAGAGCGACACGCCAGCATG
TTGGCGAAGATGGCGAGCTGCACGTCCGTGATCATCCTGACCAGTCCGGCTCGGCCCGCAGAAACCAGCACACTG
GAGCCACCGCTGCCACCGCCTT

SEQ ID NO:255

>GL2-96-5M13F Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCGCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGTCCGCAAAACCAGCAC
AGTGGTTAGATAGATAAAGC

SEQ ID NO:256

>GL2-96-5M13R Direction: N/A

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGGGA
GTAGAAAAGCAAGCCCTATACTGGGCCCTATTAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTGA
GGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCATATAAGTATGTTGTGATA

SEQ ID NO:257

>GL2_1_1_M13R Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCGCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGCGCCGATCGCGATCTAGAACTAGTCCGCAAAACCAGCAC

SEQ ID NO:258

>GL2_1_2_M13F Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCGCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGCGCCGATCGCGATCTAGAACTAGTCCGCAAAACCAGCAC

TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTCCAAACAACCTTTATTTCCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATACTAGACTTATT

5 SEQ ID NO:259

>GL2_1_2_M13R Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTATATTGGGGGGAGG
GAGTAGAAAAGCAAGCCCCTATACTGGGCCCCTATTCAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCT
10 GAGGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTG
AAGTGTGAAGGCCCTTCATACCTCCATCTTGCCCTCAGACTATGTACCTGGAACCCCTGGGGCNGAGAAAGCGCCA
CNTTCATTCTGCTTCTAGGGATCGNNAGACGGACACGATAGNTGACTAGAGAACGACAAGCAAGAA

SEQ ID NO:260

>GL2_226_1_1_M13F Direction: sense

15 GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACACGTTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTCATCCCTTC
TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTCCAAACAACCTTTTATTTCCCTCAGAGTCTTCCTAAT
CCTCATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
20 AAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:261

>GL2_226_1_1_M13R Direction: anti-sense

25 ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTATATTGGGGGGAGGGA
GTAGAAAAGCAAGCCCCTATACTGGGCCCCTATTCAGTGGCAGCTTCTTGTTCCATAGGATTAGGAAGACTCTGAG
GAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAAG
TGTCAGGCCCCCTCATACCTCCATCTTGCCCTCAGACTATGTCTGGAACCCCTGGGGCGGAGAAAGCGCCNCTTT
CATTCCTGCTTCTTGGGATTGTTGACGGCCACGTGGTGATAGAGAACGACAAGCAAGAAGAGCGANACGCCAGC
30 ATGTTGGCGAAGATGGCGAGCTGCACGTCCGTGATCATCCTGACCAGTCCAGGCTCGGC

SEQ ID NO:262

>GL2_226_1_2_M13F Direction: sense

35 GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTCATCCCTTC
TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTCCAAACAACCTTTTATTTCCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

40 SEQ ID NO:263

>GL2_226_1_2_M13R Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTATATTGGGGGGAGGGA
GTAGAAAAGCAAGCCCCTATACTGGGCCCCTATTCAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTGA
GGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAA
45 GTGTGAAGGCCCTTCATACCTCCATCTTGCCCTCAGACTATGTCTGGAACCCCTGGGGCGGAGAAAGCGCCACTT
TCATTCTGCTTCTTGGGATTGTTGACGGCCACGTAGTGATAGAGAACGACCAGCAAGAAGAGCGACGCACCA
GCATGTTGGCGAAGATGGCGAGCTGCACGTCCGTGATCATCCTGACCAGGTCCGGCATCGG

SEQ ID NO:264

>GL2_226_1_3_M13F Direction: sense

50 GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTCATCCCTTC
TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTCCAAACAACCTTTTATTTCCCTCAGAGTCTTCCTTAA
55 TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:265

>GL2_226_1_4_M13F Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
5 GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCTTCACACTTCACCTCATCCCTTC
TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATA
TAAAAATATAGACTTTTAAAAAAGGGCGCGCTCGCGATCTAGAACTAGT

10 SEQ ID NO:266

>GL2_81B_E01_G3F1 Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCTT
CTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCCG
15 CCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCTTCACACTTCACCTCATCCCTTC
ACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGNCACCTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATA
TNAAAATATAGACTTTTAAAAAAGGGCGCGCTCGCGATCTAGAACTAGT

SEQ ID NO:267

>GL2_81B_E05_G3F1 Direction: N/A

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GNCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCTTCACACTTCACCTCATCCCTTC
25 TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
TCCTATGGAACAAGAAGCTGGCACTGAATAGTGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATA
TNAAAATATAGACTTTTAAAAAAGGGGCGCGCTCGCGATCTAGAACTAGTCCGNNAGAAACCAGCA
CAGTGGTTAGATAGATAAAGCGGGCGGTGACTANTCTGAGGTCTGATACTCACTGACT

SEQ ID NO:268

>GL2_81B_E06_G3F1 Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCTTCACACTTCACCTCATCCCTTC
35 TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
TCCTATGGAACAAGAAGCTGCCACTGAATAGTGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGGCGCGCTCGCGATCTAGAACTAGTCCGNAGAAACCAG
CACAGTGGTTAGATAGATAAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTCACTGACTGTTCGTAAGGGCGAA
TTCGTTTAAACCTGCAGGACTAGTCCCTTTATGAGGGTTAAATTCTGAGCTTGCGGTAATCATGGTCA

40 SEQ ID NO:269

>GL2_1_3_M13R Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCTTCACACTTCACCTCATCCCTTC
45 TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCAATTTTCTACTCCCTCCCCCAAA
TATAAAATATAGACTTTTAAACAACAACAACAACAAGGGCGCCAGCTCGGCGATCTAGAACTAGT
CCGGCAAGAACCCAGNAACAGGGGTTAGATA

50 SEQ ID NO:270

>GL2_81B_E04_G3F1 Direction: N/A

GCCGAGCCGGACTGGTCAGGATGATCACGGACGCGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCTTCACACTTCACCTCATCCCTTC
55 CTANCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGGCACTGAATAGGGCCAGTATAGGGGCTTGCGTTTCTACTCCCTCCCCCAAT
ATAAAATATAGACTTTTAAAAAATNAAGGGNGCCGCTCGCGATACTAGAACTAGT

SEQ ID NO:271

>GL2_226_1_3_M13R Direction: anti-sense

CTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTAAAGTCTATATTTTATATTGGGGGGAGGGAG
TAGAAAAGCAAGCCCCCTATACTGGGCCCTATTTCAGTGGCAGCTTCTTGTTCATAGGATTAAGGAAGACTCTGAG
5 GAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAAG
TGTGAAGGCCCCCTCATACCTCCATCTTGCCTCAGACTATGTCTTGGAAACCCTGGGGCGGAGAAAGCGCCACTGT
TCATTCTGCTNTCTTGGGATTGTTTCGACGGNCACGTAGATGATAGAGAACGACAAGCAAGAAGAGCGAANACGC
CCAGCATGTAAGGCGAAGATGGCGAGCTGCACGTCCGTGATCATCTGACCAGTCCGGCTCGGA

10 SEQ ID NO:272

>GL2_226_1_4_M13R Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTAAAGTCTATATTTTATATTGGGGGGAGGGGA
GTAGAAAAGCAAGCCCCCTATACTGGGCCCTATTTCAGTGGCAGCTTCTTGTTCATAGGATTAAGGAAGACTCTGA
15 GGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAAG
GTGTGAAGGCCCCCTCATACCTCCATCTTGCCTCAGACTATGTCTTGGAAACCCTGGGGCGGAGAAAGCGCCACTT
TCATTCTGCTTCTTGGGATTGTTGACGGCCACGTAGTGATAGCGAACGACAAGCAAGAAGAGCGACACGCCCAG
CATGTTGGCGACGATGGCGAGCTGCACGTCCGTGATCATCTGACCAGTCCGGCTCGGCCCGAAGAACCAGACA
ACACTGGAGCCACCGTGGCCACCGGCCCTTGGCGGCTACCTCCTTGTAAGCTCGGTCCATGCCGAGAGAAGGGCG
AAATACTGCAGATATCCATCACAACCTGGCGGGCCGATCCGAGCATGCATCTAGAAGGGCCAAATACGCCATATA
20 GGNAGTCCGAATAACAATTCACCTGGCCGGCGATCCAAACGTCGTGACTGGAAAAAACCCGGGGGATNACCCAA
AAAAGTTAAATTCGGCCNGAAGGACANAACCCACGATTAGGCAANAGNGCGAAAAATAACNAAA

SEQ ID NO:273

>GL2_81B_E03_G3F1 Direction: sense

5 GCGGAGCCGACTGGTTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAGGTGGCGCTTTCTCC
GCCCCAGGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCTTCACACTTCACTTCATCCCTT
CTACCCATCACAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACTTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATA
30 TAAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:274

Clone 1/226 - Novel (Clone1/226) >

5 GCGGAGCCGACTGGTTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAGGTGGCGCTTTCTCC
GCCCCAGGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCTTCACACTTCACTTCATCCCTT
TACCCATCACAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACTTTTATTTCTCAGAGTCTTCCTTA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
40 AAAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:275

Novel (FLJ10688)

>GL2_51_C08_G3F1 Direction: sense

5 CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGA
AGCCACACTTGAAGTTAGCACGCTTCAGAGTCAAAATGGCATAGTACTGTCTATGGAGTGTCTTGGAGGTGGATC
45 GAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAAT
GGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGC
AAATACTACTTTG

50 SEQ ID NO:276

>GL2_51_C10_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCAGAAGCTGCCAGCACATCTCTGCCTCAG
AAGCCACACTTGAAGTTAGCACGCTTCAGAGTCAAAATGGCATAGTACTGTCTATGGAGTGTCTTGGAGGTGGAT
CGAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACA
55 TGGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGC
AAATACTACTTTG

SEQ ID NO:277

>GL2_51_C11_G3F1 Direction: N/A

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGA
AGCCACACTTGAAGTTAGCACGCGTTGAGGGGTCAAATGGCATAGTACTGTCATGGAGTGTCTGGAGGTGGAT
5 CGAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
TGGAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGC
AAATACTACGTTTG

SEQ ID NO:278

>GL2_59_E07_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAAA
CCACACTTGAAGTTAGCACGCGTTGAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTGGAGGTGGATCG
AAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
15 GAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGCAA
ATACTACTTTG

SEQ ID NO:279

>GL2_59_E08_G3F1 Direction: sense

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAG
20 AAACCACACTTGAAGTTAGCACGCGTTGAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTGGAGGTGGAT
CGAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
TGGAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGC
AAATACTACTTTG

SEQ ID NO:280

>GL2_59_E09_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAA
GCCACACTTGAAGTTAGCACGCGTTGAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTGGAGGTGGATCG
AAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
30 GAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGCAA
ATACTACTTTG

SEQ ID NO:281

>GL2_59_E10_G3F1 Direction: sense

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGA
35 AGCCACACTTGAAGTTAGCACGCGTTGAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTGGAGGTGGATC
GAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
GGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGCA
AATACTACTTTG

SEQ ID NO:282

>GL2_59_E11_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGA
AACCACACTTGAAGTTAGCACGCGTTGAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTGGAGGTGGATC
45 GAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
GGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGCA
AATACTACTTTG

SEQ ID NO:283

>GL2_59_E12_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAA
GCCACACTTGAAGTTAGCACGCGTTGAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTGGAGGTGGATCG
AAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
50 GAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGCAA
ATACTACTTTG

SEQ ID NO:284

>GL2_51_C09_G3F1 Direction: N/A

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAAGAACAAACAGGGCCCTTTGTGGTCG
TNCCCCACAAAAGGGGGCCCCCTTATAAACACCCATAAAATTTTTTACCCCTTTTNTCCCCCTTGGGGTGTCCCC
CCCCCTTTTTTTTCCCCAAAAAGGGGNCCCCAAAACCAAGGGGGCCCCCCCCCTTTAAAAACCCTAAAAACCC
CCTTTTTTTTTTTTTTTTNGGGGGCCCCCAACCCAAAC

SEQ ID NO:285

Novel (FLJ10688)>

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGA
AGCCACACTTGAAGTTAGCACGCGTTCAGAGTCAAAATGGCATAGTACTGTTCATGGAGTGTCTTGGAGGTGGATC
GAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCCACAAAT
GGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTACCCAGTTTGTATCTGGTAGCA
AATACTACTTTG

SEQ ID NO:286

>gi|8922591|ref|NM_018179.1| Homo sapiens hypothetical protein FLJ10688 (FLJ10688), mRNA

ATCTAAACAAGAAAGTAGTGAGAGTTTGCCAAAAGAAGCCTTTCTGGTCTCTCTGATGAAGAGGATATT
TCGGGTGAAAAAGATGAGTCTGAAGTTATATCGCAAAATGAAACGTGCTCTCCAGCAGAAGTAGAAAGTA
ATGAAAAGGACAACAGACCTGAGGAAGAAGAGCAAGTAATACATGAAGATGATGAAAGACCTTCTGAGAA
AAATGAATTTCTAGACGAAAACGTTCTAAATCAGAAGACATGGACAATGTACAGTCTAAACGTCGTCGA
TATATGGAAGAAGAATATGAGGCAGAAATTTCAAGTAAAGATTACAGCCAAAGGAGACATTAAACCAGAAAC
TTCAAAGGTTTATACAGTGGTTGCTGGAAGAAAAAATTGTGTGCGCTGCAGTGTGCTGTATTTGATAAGAC
TTTGGCAGAATTGAAAACACGAGTGGAAAAGATTGAATGTAAACAAGAGGCATAAAACAGTTCTCACTGAA
CTACAGGCCAAGATAGCCAGGTTAACCAAACGCTTTGAAGCAGCCAAAAGAAGATCTTAAGAAAAGACATG
AACATCCACCCAACCCACAGTATCACCAGGAAAACTGTAAATGATGTCAACAGCAATAATAACATGTC
TTACAGAAATGCAGGCACAGTGAGACAGATGCTGGAGTCCAAAAGAAATGTAAGCGAGAGTGCACCACCA
TCCTTTCAAACCTCTGTGAATACAGTATCTTCAACCAATCTTGTCACTCCTCCAGCAGTTGTCACTAGTC
AACCTAAATTGCAGACTCCAGTGACTTCGGGTTCCCTCACAGCAACGTCAGTTCTTCTCCTGCACCCAATAC
AGCTACTGTAGTTGCTACTACTCAGGTGCCTAGTGGAAATCCCCAGCCTACAATCTCTTTACAGCCTTTG
CCAGTGATTTTGCATGTACCTGTTGCAGTATCCTCCCAGCCTCAGTTCTACAGAGCCATCCAGGGACTT
TGGTGACTAATCAACCATCTGGCAATGTTGAATTCATTTCTGTGCAAAGCCCACCTACAGTGAGTGGTCT
TACCAAAAATCCAGTATCCTTGCCATCCTTGCCAAATCCCACTAAACCAAACACGTTCTCTGTGCCC
AGTCCTAGTATTCAAAGGAACCCCTACTGCCAGTGCTGCACCATTTGGGAACAACACTTGCTGTGCAGGCTG
TTCCAACAGCACACTCTATTGTACAAGCCACAAGGACTTCTTTACCCACAGTGGGCCCCATCAGGACTCTA
TAGTCCATCAACTAATCGAGGTCTTATACAGATGAAAATTCCAATTTCTGCATTTAGTACTTCTGTCTGCT
GCAGAACAGAACAGCAATACCACCCCAAGAATTGAAAACAGACAAACAAAACAATAGATGCTTCTGTCA
GTAAGAAAGCAGCTGATAGCACATCACAGTGTGGAAAAGCCACTGGCAGTGATTCAAGTGGTGTCTATTGA
TCTCACAAATGGATGATGAAGAGAGTGGAGCTTCACAAGACCCCAAAAACTAAATCACACTCCTGTATCA
ACCATGAGTTCTTCTCAGCCTGTGTACGACCATTGCAACCCATACAACCAGCACCAGCCTCTTCAACCAT
CTGGGGTGCCAACAAGTGGACCATCTCAGACCACCATACACTTACTACCTACAGCTCCAACCTACCGTGAA
TGTAACACATCGTCCAGTAACTCAGGTGACCACAAGACTCCCTGTACCAAGAGCTCCTGCAAAACCACAG
GTGGTTTATACAACCTCTTCTGCACCAACAGCTCAGGCTCCCTTGCGAGGAAGTGTATGCAGGCTCCTG
CTGTTCCGGCAGGTCAATCCCCAAAATAGTGTTACAGTTCGAGTGCCTCAAACAACCACATATGTTGTAA
CAATGGACTAACCCTGGGATCAACAGGACCTCAGCTCACAGTGCATCACCAGCACCACAAGTGCATACT
GAGCCCCCAGCCCCGTGCACCCAGCACCCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAG
CTGCCAGCACATCTCTGCCTCAGAAGCCACACTTGAAGTTAGCACGCGTTTCAGAGTCAAAATGGCATAGT
ACTGTCATGGGGTGTCTTGGAGGTGGATCGAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTAC
CATGAGGAACCCAGTGCCACTGTGCCCCACAATGGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGC
CCATGGCATGTACTCTCACCCAGTTTGTATCTGGTAGCAATACTACTTTGCAGTACGAGCCAAGGATAT
TTATGGACGTTTTGGGCCCTTCTGTGATCCTCAGTCAACAGATGTGATCTCTTCTACCCAGAGCAGTTAA
ACCTTGGAGCCTTTATATTTTCTCTTTTAAAAATTTCCACCTTTTGGTCTTGTTTTTAATCTTGTGCATG
ATACCCCATGTAAATCCACCTTGTGCAAGATTTCTTGGACAGATGTGTGTATACACTACATTTGTTTAT
AACCAGAAGCAAAATAAACTCAGCCCAAAAGCT

SEQ ID NO:287

>gi|8922592|ref|NP_060649.1| hypothetical protein FLJ10688; likely ortholog of mouse activating transcription factor 7 interacting protein [Homo sapiens]

5 MDNVQSKRRRYMEEYEAEFQVKITAKGDINQKLQKVIQWLLEEKLCALQCAVFDKTLAELKTRVEKIEC
NKRHKTVLTELQAKIARLTKRFEAAKEDLKKRHEHPPNPPVSPGKTVDVNSNNMSYRNAGTVRQML
KRNVSSEAPPSFQTPVNTVSSNTLVTPPAVSSQPKLQTPVTSGLTATSVLPAFNTATVVATTQVPSGN
PQPTISLQPLPVILHVPVAVSSQPQLLQSHPGTLVTNQPSGNVEFISVQSPPTVSGLTKNPVSLPLPNP
TKPMNVPSVPSPSIQRNPTASAAPLGTTLAVQAVPTAHSIVQATRTSLPTVGPSTLYSPSTNRP
10 PISAFSTSSAAEQNSNTTPRIENQTNKTIDASVSKAADSTSQCCKATGSDSSGVIDLTMDDEESGASQD
PKKLNHTPVSTMSSSQPVSRPLQPIQAPPLQPSGVPTSGPSQTTIHLPTAPTTVNVTHRPVTQVTRL
PVPRAPANHQVVYTTLPAPPAQAPLRGTVMQAPAVRQVNPQNSVTVRVPQTTTYVNVNGLTLGSGTGPQLT
VHHRPPQVHTEPRPVHPAPLPEAPQPQLPPEAASTSLPQKPHLKLARVQSQNGIVLSWGVLEVDRSCA
TVDSYHLYAYHEEPSATVPSQWKKIGEVKALPLPMACTLTQFVSGSKYYFAVRAKDIYGRFGPFCDPQST
15 DVISSTQSS

SEQ ID NO:288

Novel (KIAA0217)

>G3_4_03_PCR_G3F1 Direction: N/A

20 TCTTGCGGCAGGGTCAAAACAACATCATGGTACAACCTTCTGGTAACATGTCAGTGGGCAACAAAGTGTATGTTTT
CATGTAGTTCTATTACAAATTGGTTCCTTTGAATTTATATTACATAATACCACTTGAAACTGGAGTGAGAAGCTG
GTTACTTGCTTGCACTGCATCAGAACCAAGGTTTCTGGGGTGGCCCCCTGCAGTTCCTCCGCCAGGAGATCAAA
AAGGATGCGCTCTCTTACCATTTAAATGCCACAGTCCCTACCAACGGCTTAGTTGAAGCACAGCTCCACATCA
GCACCTTATTCCTGGCGCGGCCAGCACTGCCTCTACGAGGCCACACCTGCCTCTGCCAAGGCCACTGGCCCTCAT
25 TCATCTTCGGGGACGTTCTAGAGATATGCACCTTACAG

SEQ ID NO:289

>GL3_4.03_A_M13F Direction: anti-sense

30 CTGTAAGTGCATATCTCTAGAACGTCCCCGAGATGAATGAGGGCCAGTGGCCTTGGCAGAGGCAGGTGTGGCCT
CGTAGAGGCAGTGCTGGCCGCGCCAGGGCATCAGTGCTGATGTGGGAGCTGTGCTTCCACCTAAGCCGTTGGTAG
GGGACTGTGGCATTAAAGAATGTAGAGAGCGCATCCTTTTTGATCTCCTGGGCGGAGTGAACCTGCAGGGGCCAC
CCCAGAAACCTTGGTTCTGATGCACTGCAAGCAAGTAACCAGCTTCTCACTCCAGTTTCAAGTGGCTATTATGTA
ATATAAATTCAAAGCACATTGTGAATAGAACCTACATGAAAACATACACTTTGTGCCCCACTGACATGTTACCAG
AAGTTGTACCATGATGTTGTTTTGACCCCTG
35

SEQ ID NO:290

>GL3_4.03_A_M13R Direction: sense

40 CAGGGGTCAAAACAACATCATGGTACAACCTTCTGGTAACATGTCAGTGGGCAACAAAGTGTATGTTTTCATGTAG
GTTCTATTACAAATGTGCTTTGAATTTATATTACATAATAGCCACTTGAAACTGGAGTGAGAAGCTGGTTACTTG
CTTGCACTGCATCAGAACCAAGGTTTCTGGGGTGGCCCCCTGCAGGTTCACTCCGCCAGGAGATCAAAAAGGATG
CGCTCTCTACATTCTTAAATGCCACAGTCCCTACCAACGGCTTAGGTGGAAGCACAGCTCCACATCAGCACTG
ATGCCCTGGCGCGGCCAGCACTGCCTCTACGAGGCCACACCTGCCTCTGCCAAGGCCACTGGCCCTCATTATCT
GCGGGGACGTTCTAGAGATATGCACCTTACAG

55 SEQ ID NO:291

>GL3_4.03_B_M13F Direction: sense

CAGGGGTCAAAACAACATCATGGTACAACCTTCTGGTAACATGTCAGTGGGCAACAAAGTGTATGTTTTCATGTAG
GTTCTATTACAAATGTGCTTTGAATTTATATTACATAATAGCCACTTGAAACTGGAGTGAGAAGCTGGTTACTTG
40 CTTGCAGTGCATCAGAACCAAGGTTTCTGGGGTGGCCCCCTGCAGGTTCACTCCGCCAGGAGATCAAAAAGGATG
CGCTCTCTACATTCTTAAATGCCACAGTCCCTACCAACGGCTTAGGTGGAAGCACAGCTCCACATCAGCACTG
ATGCCCTGGCGCGGCCAGCACTGCCTCTACGAGGCCACACCTGCCTCTGCCAAGGCCACTGGCCCTCATTATCT
GCGGGGACGTTCTAGAGATATGCACCTTACAG

SEQ ID NO:292

55 >GL3_4.03_B_M13R Direction: anti-sense

CTGTAAGTGCATATCTCTAGAACGTCCCCGAGATGAATGAGGGCCAGTGGCCTTGGCAGAGGCAGGTGTGGCCT
CGTAGAGGCAGTGCTGGCCGCGCCAGGGCATCAGTGCTGATGTGGGAGCTGTGCTTCCACCTAAGCCGTTGGTAG
GGGACTGTGGCATTAAAGAATGTAGAGAGCGCATCCTTTTTGATCTCCTGGGCGGAGTGAACCTGCAGGGGCCAC
CCCAGAAACCTTGGTTCTGATGCACTGCAAGCAAGTAACCAGCTTCTCACTCCAGTTTCAAGTGGCTATTATGTA

ATATAAATTCAAAGCACATTGTGAATAGAACCTACATGAAAACATACACTTTGTTGCCCACTGACATGTTACCAG
AAGTTGTACCATGATGTTGTTTTGACCCCTG

SEQ ID NO:293

5 >GL3_4.03_C_M13F Direction: anti-sense
CTGTAAGTGCATATCTCTAGAACGTCCCCGAGATGAATGAGGGCCAGTGGCCTTGGCAGAGGCAGGTGTGGCCT
CGTAGAGGCAGTGTCTGGCCGCGCCAGGGCATCAGTGTCTGATGTGGGAGCTGTGCTTCCACCTAAGCCGTGTTAG
GGGACTGTGGCATTTAAGAATGTAGAGAGCGCATCCTTTTTGATCTCTCTGGGCGGAGTGAACCTGCAGGGGCCAC
10 CCCAGAAACCTTGGTTCTGATGCACTGCAAGCAAGTAACCAGCTTCTCACTCCAGTTTCAAGTGGCTATTATGTA
ATATAAATTCAAAGCACATTGTGAATAGAACCTACATGAAAACATACACTTTGTTGCCCACTGACATGTTACCAG
AAGTTGTACCATGATGTTGTTTTGACCCCTG

SEQ ID NO:294

15 >GL3_4.03_C_M13R Direction: sense
CAGGGGTCAAACAACATCATGGTACAACCTTCTGGTAACATGTCTAGTGGGCAACAAAGTGTATGTTTTTCATGTAG
GTTCTATTACAAATGTGCTTTGAATTTATATTACATAATAGCCACTTGAAACTGGAGTGAGAAGCTGGTTACTTG
CTTGCACTGCATCAGAACCAAGTTTTCTGGGGTGGCCCTGCAGGTTCACTCCGCCAGGAGATCAAAAAGGATG
CGCTCTCTACATTCTTAAATGCCACAGTCCCTACCAACGGCTTAGGTGGAAGCACAGCTCCACATCAGCACTG
20 ATGCCCTGGCGCGGCCAGCACTGCCTCTACGAGGCCACACCTGCCTCTGCCAAGGCCACTGGCCCTCATTCATCT
GCGGGGACGTTCTAGAGATATGCACTTACAG

SEQ ID NO:295

25 >GL3_4.03_D_M13F Direction: anti-sense
CTGTAAGTGCATATCTCTAGAACGTCCCCGAGATGAATGAGGGCCAGTGGCCTTGGCAGAGGCAGGTGTGGCCT
CGTAGAGGCAGTGTCTGGCCGCGCCAGGGCATCAGTGTCTGATGTGGGAGCTGTGCTTCCACCTAAGCCGTGTTAG
GGGACTGTGGCATTTAAGAATGTAGAGAGCGCATCCTTTTTGATCTCTCTGGGCGGAGTGAACCTGCAGGGGCCAC
CCCAGAAACCTTGGTTCTGATGCACTGCAAGCAAGTAACCAGCTTCTCACTCCAGTTTCAAGTGGCTATTGTGTA
ATATAAATTCAAAGCACATTGTGAATAGAACCTACATGAAAACATACACTTTGTTGCCCACTGACATGTTACCAG
30 AAGTTGTACCATGATGTTGTTTTGACCCCTG

SEQ ID NO:296

35 >GL3_4.03_D_M13R Direction: sense
CAGGGGTCAAACAACATCATGGTACAACCTTCTGGTAACATGTCTAGTGGGCAACAAAGTGTATGTTTTTCATGTAG
GTTCTATTACAAATGTGCTTTGAATTTATATTACAAATAGCCACTTGAAACTGGAGTGAGAAGCTGGTTACTTG
CTTGCACTGCATCAGAACCAAGTTTTCTGGGGTGGCCCTGCAGGTTCACTCCGCCAGGAGATCAAAAAGGATG
CGCTCTCTACATTCTTAAATGCCACAGTCCCTACCAACGGCTTAGGTGGAAGCACAGCTCCACATCAGCACTG
ATGCCCTGGCGCGGCCAGCACTGCCTCTACGAGGCCACACCTGCCTCTGCCAAGGCCACTGGCCCTCATTCATCT
GCGGGGACGTTCTAGAGATATGCACTTACAG

40 SEQ ID NO:297

>gi|22051279|ref|XM_040265.5| Homo sapiens KIAA0217 protein (KIAA0217),
mRNA
AGCATCCTGAGGTTAGCATTACACTTCTCCAGTGGAGCCCATGACTTCTGATCAGGACGCTAAGGTTGT
GGCTGAACCGCAGACGCAGAGAGTCCAGGAGGGCAAGGACAGCGCTCATCTGATGAATGGTCCTATATCT
45 CAAACCACTTCTCAGACAAGTTCATCCCACCTTTGAGTACCAGCAACTAAGGTTTCAGAGCTGA
ACCCTAATGCAGAAGTGTGGGGGGCTCCTGTGTTACATCTGGAAAGCAAGCAGTGTCTGCTGACGGTGTGAG
TGCTGCATGGGAGGAGGTGGCTGGCCACCACGCAGACCCGTGGCCCGCAGGGATCGGATGCCAATGGTGTAT
GGTGACCAGGGCCATGAGAAATGCCGATTTGCCAGACCCGAGGAGTCCGACCCAGCAGACATGAACGCTC
TCGCTCTGGGTCCCTCAGAATATGACTCTCTGCCTGAAAATAGCGAGACAGGAGGAAATGAGTCTCAACC
50 AGACAGCCAGGAAGACCCCCGAGAAGTACTTAAAAAAACATTTGGAATTCTGCTTATCTAGGGAGAACCTT
GCTAGTGACATGTATCTTATATCACAGATGGATAGTGACCAGTATGTGCCAATCACAACGGTGGCTAACC
TCGACCACATCAAGAAGCTCAGCACTGATGTGGACTTGATTGTGGAAGTGCTAAGATCTTTACCTTTAGT
CCAAGTGGATGAAAAGGGAGAAAAGTAAGGCCAAATCAAAATCGCTGCATAGTAATATTGCGTGAAATA
TCTGAATCTACCCCCGTGGAAGTAATAGAAAGCACTATTTAAAGGAGATAATTTACCAAATTTATAAACT
55 GTGAATTTGCATATAATGATAATTGGTTTATTACATTTGAAACAGAAGCTGATGCACAACAGGCTTACAA
ATACCTTCGAGAAGAAGTCAAAACTTTTCAAGGAAAACCAATTAAGGCACGGATAAAAGCAAAGGCAATA
GCTATAAACACATTTTTTGCCAAAGAATGGATTTAGACCCCTGGACGTGAGCCTGTATGCCAGCAGCGCT
ACGCGACGTCGTTCTACTTCCCTCCCATGTACAGCCCCCAGCAGCAGTTCCCCCTGTACAGCCTGATCAC
TCCCAGACGTGGTCAGCAACGCACAGCTATCTTGACCCACCCTTGGTAACTCCATTTCCAAATACTGGA
60 TTTATAAATGGGTTTACGTCTCCAGCGTTCAAGCCTGCGGCGTCTCCTCTGACTTCTCTCAGACAGTATC

CTCCTCGAAGCAGGAATCCTAGTAAATCTCATCTGCGGCATGCGATTCCCTAGTGCAGAGAGGGGACCTGG
GTTATTAGAAAGTCCTTCAATATTTAACTTCACTGCAGATCGATTAATTAATGGTGTCCGGAGTCCACAA
ACAAGGCAAGCAGGTCAAAC TAGAACACGGATTCAAACCCCTTCAGCATATGCCAAGAGAGAGGCTGGGC
CTGGGCGTGTGGAGCCAGGCAGTCTCGAATCCTCTCCTGGTTTAGGGAGGGGAAGGAAGAATTCCTTTTGG
5 CTACCGGAAGAAAAGGGAGGAGAAGTTTACAAGCAGCCAGACACAGTCTCCAACGCCACCAAAGCCTCCG
TCGCCAAGCTTCGAGCTGGGGCTGTCCAGCTTCCCTCCATTACCTGGAGCTGCCGGCAATTTGAAGACAG
AGGACTTGTGTTGAAAACAGGCTATCTAGCTTGATAATAGGACCATCCAAAGAAAGGACCTCAGTGCAGA
CGCAAGCGTGAACACCTTTCCTGTAGTGGTCTCCAGAGAGCCCTCGGTGCCGGCTTCTTGTGCTGTATCA
GCAACGCTACGAGCGATCCCCCTCCCAGCTCATTTACCCGATGATCCCAAGGTGGCGGAGAAACAGAGGG
10 AAACCCACAGTGTGACAGACTTCTTCCGCCCTCACTGCGACCGCGTGTAATCGGTGCAGGTGAACGG
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TCCCCATTGCAACCCCAAAGAACAAGCCAAACACTGTTGGTTGTGGGAAGGAGGAAAAGAGCTGG
CAGAGCCCGCAGAGAGATACCGGGAGCCCCAGCCCTCAAGTCCACACCTGGAGCCCCCAGAGACCAGAG
GCGGCCGG
15 CCAAAGTCTCCTCAGTGAACCCGTACGCTCGGGAGGGGTGCGAGAGCGCTGTGTTAACCACAAACGAGA
CACTCTCCCACTCAGTGCAGAGGGCGAGCCGCTGGTTAGGAGCTTGCAGTGTCTGAGGCCCTGTGGGATCCT
CAAGTTGGTTTTCTTCTGTGAGTTGGATTCTCCCCCTCTTGAAAAAAAATCGATTTTTTTCAGGATTTAATT
AATACAAACCTTATTTTAGGTTGGTGCTTAACTGGAGGTGATGCATAAGTCTGATTTTTTTTTTCCAAGAT
AGAAAAAGCATTATCCTTAACAAATTGGTATTTTTTATTAAGCCTCCATGTGGCTCTGAATGCAAGCTAT
20 ATATAGTGAGTTTTTCTAAATTAAGGGAACCTCGCTTTTTTTTTTTTTTTTTTTTAAAGTAACTGGTCTGTAA
TGCATATCTCTAGAAGCTCCCCGCAGATGAATGAGGGCCAGTGGCCTTGGCAGAGGCGAGGTGTGGCCTCG
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TAGGGGACTGTGGCATTTAAGAATGTAGAGAGCGCATCCTTTTTGATCTCCTGGGCGGAGTGAACCTGCA
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25 TGGCTATTATGTAATATAAATTCAAAGCACATTTGTGAATAGAACCTACATGAAAACATACACTTTGTTGC
CCACTGACATGTTACCAGAAGTTGTACCATGATGTTGTTTTGACCCCTGTGAGCTGATGGCCCCGGCCCT
GCTCTGTGCACATTTCTGTCCGTGTTCCCCAGCACTCTGGTTGGAGAGAGTCCACATCTTCAGCTCCGTG
TGGACATCTCCCTGTACCTCTGCATCAGCATGGATTAAGAGTTATGTAATCGTGAGAGAATGGTGTT
TGTGGTTTTTCCCCCTCTTTGGCTGGTGGAGGATAAAGTTTCTGCTCTTTTACCTCCAAGACGAGGGCCT
30 CATTGATTCACCTCCAGAAAGTGCTGCACCTCTGAAGAACAAGGATGCACCTAAAGTTAGCAAGTTTTATAAT
AAAGTTAAATATAAATTTATTTGTTTTTAAATGCCCTCAAATTTTTCTTTATTTCTAAGCAGCAAAACATTAA
AATAAGAATATTTCTGCTAAATGTAACCATAACCTTTATTCACAAAATGTTATTTAACAAGACTGAGG
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35 CAGAGTTACTCAGTTACTGCGTGGATCTCCTGTGCGTAGTTTTACTGAGTAAGCATACTGTAGTACAAGA
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AATGTTGCTGTTGAGCGGGATGTAGATAAACTAAATGTTGTGGTTTGAATATTTATTTGATTTGTTGAGA
40 TTTTCTTTTTTCTTACATCGGTGTGTTGAAGTATTCTGCCCTCTTTGCTGCAAAAGGGAATTGGAAAG
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45 AAGAACATGGGGATTTTTTTTTGTAGTTGTGAGTTCACTGACCAAAAAAAAAAAAAAAAAATCAGAAATAAT
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50 GCAGCGCGTGCATTAGCCAGTCGCCACTGGAGGGCTCTGCTGCCCTCCGGTCAATACACTGTAGTTACTG
CCTAGCCAGCAGCAGTCTTCTGCATCAAGAACTGAAACGTTGCTCGGAGGTGATTTTTATAGCATCCTTT
TTAATTAAGGTGAAATACAGATTGCTATATAATGTCTGAAAAACCTGATACTACTTCAAGAGTTTCTG
CTCAGAAGAAAAATGAGAGTTATCATAATAGGAAGCTGTGGCGGTCCATGCCAACTGTGCTGTGTACATA
CAGCGATGAGAGTGGCTTTTCTACTTTTTTTTTTTTAAAGTTAACACCCCTCCTTTACCCCGCAGCATC
55 TCAGGTTATAGAATCAGAGATGCAGCAGTGACAAATGGCATTTTAACTTGTAAATCGTGTGATGAGTCT
TATCATTTTGAATAGAAGAATAAAAAACCTGGTCCCGTTTACCAGACATGAATTTCAAGTGGAGTCTGTC
GTTCTCTGAGAGTGAAGTGTCTTGACATTTTACCCAGGCCCTCCTGTCTCATCACATCACCGGCTGTCACTG
GCGGGTGGCCGTAAACGTCCTGCGTTGCTATATTAGGATCTCTGCAGTTCAAGGCTTCAAACACAGTTTCA
TGTATCCGGGCGACGGGTAGTGGTGGTGCATGCCTGTCTGTGTGCCCCGCTGGCGAGCTGTAGTTGCGGC
60 TTGCGTGCCTCGCGGGCCACTACAGGGCTGCAGACAATCGAGGCGAGGGCGCTGGCCGCCAGCAGCTCAC
AGCGCGGGGGTCATGTGGTCTCCTCGAGGGTTTCGTTTTTGTCTGCTTCATTAAAGACTGGAATCAAG

CTTACATGTAACTATTGGTAATTTAAGTTTCCTTTTGTGTGCATTTCAGTGTAAACTGTCTAATTTGAAA
AAAAATGTAGGTTATGAAAATAAAGATTTAGGCACTGTTTC

SEQ ID NO:298

5 >gi|20543999|ref|XP_040265.4| similar to no similarities to reported gene
products [Homo sapiens]
MTSDQDAKVVAEPQTRVQEGKDSAHLMNGPISQTTSTSSIPPLSQVPATKVSSELNPNAEVWVWAPVLHL
EASSAADGVSAAWEEVAGHHADRGPQGS DANGDGDQGHENAALPDPQESDPADMNALALGPSEYDSL PEN
10 SETGGNESQPDSDQEDPREVLKKTLEFCLSRNLASDMYLI SQMDS DQYVPIITTVANLDHIKKLSTVDLI
VEVLRSLPLVQVDEKGEKVRPNQNCIVILREISESTPVEVIEALFKGDNLPKFINCEFAYNDNWFITFE
TEADAQQAYKYLRREEVKTFQGKPIKARIKAKAIAINTFLPKNGFRPLDVSLYAQQRYATSFYFPPMYSPO
QFPLYSLLTPQWTSATHSYLDPLVTPFPNTGFFINGFTSPAFKPAASPLTSLRQYPPSRNPSKSHLRH
AIPSAERGPGLLESPIFNFTADRLINGVRSPQTRQAGQTRTRIQNPSAYAKREAGPGRVPEPGSLESSPG
15 LGRGRKNSFGYRKKREEKFTSSQTSPTPPKPPSPSFELGLSSFPPLPGAAGNLKTEDLFENRLSSLIIG
PSKERTLSADASVNTLPVVVSREPSVPASCASVATYERSPSPAHLPDDPKVAEKQRETHSVDRLPALTA
TACKSVQVNGAATELRKPSYAEICQRTSKEPPSSPLQPKQKPNVTGCGKEKKLAEPARYREPPALK
STPGAPRDQRRPAGGRPSPSAMGKRLSREQSTPPKSPQ

SEQ ID NO:299

20 Novel (KIAA1583)
>GL2_89_2B04_G3F1 Direction: N/A
ACTGCAGGTGGCAGCACGGGCGCGCCGCTCGGGCTCATCTGACGCCTCTGCAGCGGGTCCGCGAGGCCTGCAGGG
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25 CGTCCCCGGCGGCTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATCCGCCCTCTTGGGGTCAGGCC
TTCCACCTGCAGTGCAGCGCGCCAGCCACTCCGACTGGCGCTATGCCTCGATCACCGCTCTTGCTCCCAAGTG
GACCGCAGGGTGAGACGCTCTCTTACGTGGGACCCCTGGGTGTGCGCTCACTCTCTGAAGGGCCTGGAAGCTAGAT
TCCAGAGGCGTGGGCCAACTCTCCCTGGGTTTTTGGGTGAGCCCCCTCCGAGGGTGTTTATTCTGAGCTCTGT
GTCATCTTAAGCTCTGAGGGTNCGNAGAAACCAGACAGTGTTAGATAGATAAAGCGGGCGGTGGAATAATCTGA
30 GGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTACGGGGCGNTAAAATTCNAATTGCCTATAGTGAGTCTGTA
TTACAAATTCACCTGGCGCGGTTTTACAAANGTCGTGACTGGGAAAACCTGGCGTTACCCAACTTAATCGCTTGA
GGAATCCCCCTTTTCGAGTGGGGTATAGGAGAAGGCGACGAATGCCTCCAACAGTGGGCAGCNAAGTACGACGGT
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GGATTG

35 SEQ ID NO:300

>GL2_202_3_M13F Direction: anti-sense
ACCCTCAGAGCCTAAGATGACACAGAGCTCAGGAAATGAACACCCTCGGAGGGGGCTCCCCAAAACCCAGGGGAG
AGGTGGCCACGCCTCTGGAATCTAGCTTCCAGGCCCTTTTTCAGAGAGTGAGCGCCCCCAGGGGTCCCCGTAAG
40 AGAGCGTCTCCCCTGCGGTCCACTTGGGAGCAAGAGCGGTGATCGAGGCATAGCGCCAGTCCGGAGTGGGCTGGG
GCGGCTCGCCTGCAGGGTGGAAGGGCCTGACCCCAAGAGGGGCGGATGTCTGCGTTTTGAGAAACAGGAGCTGCT
GGTGATTAGGAGCCGCCGGGGACGAGCTGCGGGTCT

SEQ ID NO:301

>GL2_202_3_M13R Direction: sense
45 ACTGCAGGTGGCAGCCACGGGGCGGCCGCCCCGGGTGCGGCTCATCTGACGCCTCTGCAGCGGGTTCGCGAGCCT
GCAGGGCGGGGAGGCCGGGACTGGCCGTGAGCGCTGAACGGGCCAGCCTGCCAGGGCCAGCTGCTGGAGACCCG
CAGCTCTGTCCCCGGCGGCTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATTGCCCCCTCTTGGGGT
CAGGCCCTTCCACCTGCAGGCGAGCCGCCAGCCACTCCGACTGGCGCTATGCTC

50 SEQ ID NO:302

>GL2_89_2B01_G3F1 Direction: sense
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GTGGGCGGGAGTGC CGGACTGGCCGTGAGCGCTGAACGGGGCCAGCTGGCCAGGGGCCAGCTGCTGGAGACCC
GCAGCTCGTCCCCGGCGGNTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATTGCCCCCTCTTGGGG
55 TCAGTGCGCCTTCCACCTGCAGTGCGAGCCTGGCCCGAGACCCTCCGACTGGCGCTATGCCTCGATCACCGGTC
TTGCTCCCAAGTGGACCGCAGGGTGAGACGCTCTCTTACGGGGACCCCTGGGGGCGCTCACTCTCTGAAGTGGCCT
GGAAGCTATGATTCCAGAGGCGTGGGCCAACTCTCCCTGGGTTTTGGGGAGCCCCCTCCGAGGGTGTTTATTATC
CTGAGCTCTGGTGTCTATCTTAGGCTCTGAGGGTCTGCGAGAAACCAGGCACCAAGTGGTTAGATAGATAAAGCTGG
60 GCGGTGCACATAGATCTGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTC

SEQ ID NO:303

>GL2_89_2B02_G3F1 Direction: sense

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5 CTCGTCCCCGGCGGGCTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATCCGCCCCCTCTTGGGGTCAGG
CCCTTCCACCTGCAGNGCGAGCCGCCAGCCCACTCCCGACTGGCGCTATGCCTCGATCACCGCTCTTGCTCCC
AAGTGGACCGCAGGGGAGACGCTCTCTTACGGGGACCCTGGGGGCGCTCACTCTCTGAAGGGCTGGAAGCTAGA
TTCCAGAGGCGTGGGCCACCTCTCCCTGGGTTTTGGGGAGCCCCCTCCGAGGGTGTTTCATTTCTGAGCTC

SEQ ID NO:304

>GL2_89_2B03_G3F1 Direction: sense

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GGGAAAAACCTGGCGTTACCCAACTTAATCGCCTTGACGACATCCCCCTTTCGAGCTGGCGTAAATAGCGAAGA
15 GGCCCGACCGATCGCCTCCCAACAGTGCAGCTATACGTACGGGAGTAAGGGTNCACCTATNAAGAAANAGCGAC
CGCCGGTGGGCGNCACCACAGGGACAANAATGGACGCACGANCAACGAACGTCACCCAGAACAGAACTAGTCA
AAAAANCCGAAAAACNGAGAGACTAAGGAAAAANNCAAAACAAAAACACAAGAAAACCAACC

SEQ ID NO:305

>GL2_89_2B05_G3F1 Direction: N/A

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GCTCGTCCCCGGCGGCTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATCCGCCCCCTCTTGGGGTCAG
GCCCTTCCACCTGCAGGCGAGCCGCCAGCCCACTCCCGACTGGCGCTATGCCTCGATCACCGCTCTTGCTCCC
25 AAGTGGACCGCAGGGGAGACGCTCTCTTACGGGGACCCTGGGGGCGCTCACTCTCTGAAGGGCCTGGAAGCTAGA
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TCATCTTAGGCTCTGAGGGT

SEQ ID NO:306

>GL2_89_2B06_G3F1 Direction: N/A

ACTGCANGTNGNAGCCACGGGCGCGCCGCTCGGGCTCATCTGACGCCTCTTTTCAGCGGGGTTCCGCAGTGCCTG
CAGGGGCGGGGAGTGCCGGGACTGGGCGTCAGCGCTGAAAGGGGCCAGCTGTCCAGTGGGGCCAGCTGCTGGAGAA
ACCGCGAGGNGTCTGGTTCCCGGCGGGGTCCTAAGTNACCAGCAGAGNGTCTGGTTTTCTCAAACGCAGACAT
TCTGGCCCTCTTGGGGGTGAGGGCCTTTACCTGTCAGGCGAGCCCGCGCCAGNGGCCGACGGTCCCCGAAACAT
35 GGGGCGGCGTAATTGTCTTCTCGAATCTAAACAGCGGTCC

SEQ ID NO:307

Clone 89 -Novel (KIAA1583)>

ACTGCAGGTGGCAGCCACGGGCGCGCCGCTCGGCCTCATCTGACGCCTCTGCAGCGGGTTCCGCAGGCCTGCAGG
40 GCGGGGAGGCCGGGACTGGCCGTACGCGCTGAACGGGCCAGCCTGCCAGGGGCCAGCTGCTGGAGACCCGCAGC
TCGTCCCCGGCGGGTCTTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATCCGCCCCCTCTTGGGGTCAGG
CCCTTCCACCTGTCAGGCGAGCCGCCAGCCCACTCCCGACTGGCGCTATGCCTCGATCACCGCTCTTGCTCCC
AAGTGGACCGCAGGGGAGACGCTCTCTTACGGGGACCCTGGGGGCGCTCACTCTCTGAAGGGCCTGGAAGCTAGA
TTCCAGAGGCGTGGGCCACCTCTCCCTGGGTTTTGGGGAGCCCCCTCCGAGGGTGTTTCATTTCTGAGCTCTGTG
45 TCATCTTAGGCTCTGAGGGT

SEQ ID NO:308

>gi|10047240|dbj|AB046803.1| Homo sapiens mRNA for KIAA1583 protein,
partial cds

GTGGTGAGAGGGGAAGGGACATTTACAGCCCTTTTCTCCCTCCCTTGCCACAACCTACTGTGCCCCAGCA
TGGCACCCGGGTGAGCCCTGCCAGCTCTGGAGCTGTATCATCTCTCCCTCTTATGCCCTCTTCAGTGGA
CTGTGGCCAGGCTCCCTTGACCTGTCTACCTGCCGGCAGCCCTGGAGCTCCTAGACGCCCCGTAACAC
TTCCGTGTGCAGCAGGTGGGCCACTACCCACCTGCCAACTCCTCTCTGAGCTCCCGATCTGAGACCTTTC
TGCTCTACAGCCCTGGGCCAGGGCCAGCCACTTCTCCGGGCTCCTACCCACCTTTTGCCACTCAGCA
55 GTTGTGTCCTCCCTCGAGTCACTGAGCCCAACGAGCCAGTCCCATGGGACGTGCGGGCCGTTTCAGTG
GAAGCGGCTGTGACTCCAGCAGAGCCCTACGCCCCGCTCTCTTCCACCTCAAAGGGCAGGATTGGCCAC
CAGGGTCTGGCAGCCTGCCCTGTGCCCGGCTCCATGCCACACACCCTGCCGGCACTGCTCACCAGCCCTG
CCGCTTCCAGCCATCCCTGGGCGCCTGCGTGGTGGAGCTGGAGCTTCCCTCGCACTGGTTCTCACAGGCC
TCCACCACAGGGCCGAGCTGGCCTACACGCTTGAGCCTGCAGCTGAGGGCCCTGGGGGCTGTGGCTCCG
60 GCGAGGAGAACGACCTGGGGAGCAGGCCCTCCAGTGGGGGGTGTGGAGCTGCGCCAGCAGACCCCCC

GCAGTACCAGGAGGTACCTCTGGACGAGGCTGTGACTCTGCGGGTGCCTGACATGCCAGTGCGGCCCCGGC
CAGCTCTTTAGTGCTACCCCTCTGCTTCGGCACAACTTCACAGCCAGCCTCCTGACCCTGCGGATCAAGG
TGAAGAAGGGGCTGCATGTGACAGCCGCCCGCCAGCCAGCCACACTCTGGACTGCCAAGCTGGACCG
CTTCAAGGGCTCCAGGCACCACACCCTCATCACCTGCCACCGTGTGGGCTCACAGAGCCAGATTCC
5 AGTCCCCCTGAAGTGTCTGAGTTCCTATGGGTGGACTTTGTGGTGGAGAATAGCACTGGTGGGGGCGTAG
CGGTCACTCGCCCCGTACAGTGGCAGCTGGAGTACCCAGGCCAGGCCCTGAAGCAGAGAAGGACAAAAT
GGTGTGGGAAATCCTGGTGTCTGAGCGGGACATCAGAGCCCTTATCCCACTGGCCAAGGTAAGGAGACCT
CCATCTCTGCCTGGGAAGGCTGGAGGCCAAGTCCCAGGAGCCCCATGAGCTGAGGGGCTGGGGCTGAGC
10 CCTCCTCCACCCCCAGGCTGAGGAGCTGGTGAATACAGCACCCTGACTGGAGTGCCCCAGCATGTCCC
CGTGCCTCTGTCACTGTGGACGGCGGGGGGCCCTTGGTGGAGGTGACAGAGCATGTGGCTGCGAGTCT
GCCAACACACAGGTCCTGCGAGGTGAGTGGCAGGTGCCAGCTCATGTGAGTCTGCATTGTGTGGGCACA
GTTACGCACACACACCTTTCTCCTTCTCATGTGGGTCCCCAAGAGAACAGCTTCTTCTTGAGACGAGA
AACCTCATGGGAGGAACCACAGCTTCAACTTCTTTTGTTCAGCCACCTCTCTCCGAGTCAAGTAACCC
15 TAACAGCCCCCGACCTTAGACACTTTCAGCTCATTATTGCACTGGCAAGTGCGCTGGCCTGAGAGAGT
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TCATGGGCTGGTCTCTTAACCTCTCTGAGCCTCGTTACCTAACTTTAAAATGAGAACATATCTTCGGGT
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20 GAAGTGAATAAAAAGGGAGGGTGGTAGAGCAACTTCTCTATCTTGAAGTTCTAAGAGGGGAAGCATGGA
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25 ACCTCAAGGAATGGCCCCCTACAGTAAATCTTAAACAAAGAACAGGGGCTTAACCAACAATCCTGCTGCA
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30 AGAGAGGGAGTTTTGCCATGTTGCCAGGCTGGTCTCAAACCTCCTGGACTCAAGCGATCCACCCACCTCG
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CAAGGAGAGCCGGGGCGCCCCGGGGGTGCGAGTGGACTTCTGGTGGCGCCGGCTCCGCGCTCGCTGCGG
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35 GCTGGAGGGTACCTGGCCCTGCTGAAGGGTGAAGTGGAGGCCTGAGGAAGCTGGCAGGCCTTGGCGAGTCA
CACTGGGACGAGAGGGCGCAGGGGACACAGCCATGGGCCCCAAGTGGGGTCAAGAAAACTGCCCTGTTG
CTTGCAAGTTCTTCTGCCCACCTCCACCTGGGCGGCCCAATGATCGCTTTCTGTGAAATTGCTGA
CTTCCGCATCCCTCTCCTCCTTCCCTCACTTCTCCGTAAGCCTCCACTTCTTAATCTACGTCA
GTACTGGTTAATGTTGCTGTCCATCCTTTCCACGCTCCTCCCCGAGAATGTACAGCCCCCTTGAAGTGC
40 GGTCTGTCTATGCTGGTGTGCTACCTCAGAGCCTAAGATGACACAGAGCTCAGGAAATGAACACCCCTCGGA
GGGGGCTCCCCAAAACCCAGGGAGAGGTGGCCACGCCTCTGGAATCTAGCTTCCAGGCCCTCAGAGAG
TGAGCGCCCCCAGGGTCCCCGTAAGAGAGCGTCTCCCTGCGGTCCACTTGGGAGCAAGAGCGGTGATCG
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45 CAGCAGCTGGGCCCTGGGCAGGCTGGGGCGGCTCAGCGCTGACGGCCAGTCCCGGCTCCCGCCCTGCA
GGCCTGCGGAACCCGCTGCAGAGGCTCGGATGAGGCCGAGCGGCGCGCCCGTGGCTGCCACCTGCAGTA
CCAGCGGGCCGGTGTGCGCTTCTCGCCCCCTTCGCGGCCACCCGCTGGACGGCGGCCG

SEQ ID NO:309

>gi|10047241|dbj|BAB13409.1| KIAA1583 protein [Homo sapiens]
50 VVRGEGTFTALFSLPCPQLLCPSPMAPGSAPASSGAVIISPSYASSVDCQAPLDPVYLPAALELLDAPEH
FRVQQVGHYPANSSLSRSETFLLQLQPWPRAQPLLRASYPPFATQQVVPVRVTEPHQRPVPWDVRAVS
EAAVTPAEPYARVLFHLKQDWPFGSGLPCARLHATHPAGTAHQACRFQPSLGACVVELELP SHWFSQA
STTRAEALAYTLEPAAEGPGGCGSGEENDPGEQALPVGGVELRPADPPQYQEVPLDEAVTLRVPDMPVRPG
QLFSATLLLRHNFTASLLTLRIKVKKGLHVTAARPAQPTLWTAKLDRFKGSRHHTTLITCHRAGLTEPDS
55 SPLSEFLWVDFVVENSTGGGVAVTRPVTWQLEYPGQAPAEKDKMVWEILVSEIRDIRALIPLAKVRRP
PSLPGKAGGQVPGAP

SEQ ID NO:310

Novel (KIAA1814)

>GL2_75_2_M13F Direction: sense

CTGGACGGCCTGGCTGGGCTGAAGGGCGAGGACAGCCGAGCAAGGAGGCAGGGGAGGGCGGCCTACCGCTGTGC
GGGCCCACGGACAAGACCCCACTGCTGAGCGGCAAGGCCGCCAAGGCCGGGACCGCGAG

SEQ ID NO:311

>GL2_75_2_M13R Direction: anti-sense

CTGCCCATGGCGTGCAGTTGGTCAGTCTGGTGGCAGCGGACGACACGTGCACCATGGCCTGCGGGCGGCCGAC
AGAGCTGAACAGCGACTGCAGCACGGAGGAGCCGGCCACGGAGCCGAGGTTGGCCTGCAGGGACATGGGGCCGAG
CGCGAACTGCGGTCCCCGGCGGGAAGGGGCCAGGAAGGACCGGTGCGTCTGGGCGGAGGACGCCGCGCCGCTGC
GGAGGACGCCCGCGGGGCCAGGCCGGGGCCGCTGAGGAGGCTTCGGGAGGCACGGCCGCGCAGAGATGAAGAG
GTTGTGGCCATTCTTGAGGTGACCTCGCGGTCCCGGGCCTTGCGGGCCTTGCCGCTCAGCAGTGGGGTCTTGTC
CGTGGGCCCGCACAGNGGTAGGCCGCTCCCTGCTCCTTGCTGCGGCTGTCTCGCCCTTCAGCCAGCCAGG
CCGTCCAG

SEQ ID NO:312

>GL2_75_3_M13R Direction: anti-sense

CTGCCCATGGCGTGCAGTTGGTCAGTCTGGTGGCAGCGGACGACACGTGCACCAAGGCCTGCGGGGCGGCACAGA
GCTGAACAGCGACTGCAGCACGGAGGAGCCGGCCACGGAGCCGAGGTTGGCCTGCAGGGGACATGGGGCCGAGCG
CGAACTGCGGTCCCCGGCGGGAAGGGGCCAGGAAGGACCGGTGCGTCTGGGCGGAGGACGCCGCGCCGCTGCGG
AGGACGCCCGCGGGGCCAGGCCGGGGCCGCTGAGGAGGCTTCGGGAGGCACGGCGCCGCGAGAGATGAAGAGGTT
GTGGCCATTCTTGAGGTCGACT

SEQ ID NO:313

>GL2_81A_D07_G3F1 Direction: N/A

CTGGACGGCCTGGCTGGGCTGAAGGGCGAGGACAGCCGAGCAAGGAGGCAGGGGAGGGCGGCCTACCGCTGTGC
GGGCCCACGGACAAGACCCCACTGCTGAGCGGCAAGGCCGCCAAGGCCCGGGACCGCGAGGTGACCTCAAGAAT
GGCCACAACCTCTTCATCTCTGCGGCGGCCGTGCCTCCCGGAAGCCTCCTCAGCGGCCCCGGCCTGGCCCCGGCG
GCGTCCCTCCGCGAGGCGGCGCGGCTCCTCCGCCAGACGCACCGGTCTTCTTGGGCCCCCTTCCGCGGGGACCG
CAGTTGCGGCTCGGCCCATGTCCCTGCGAGGCCAACCTCGGCTCCGTGGCCGGCTCCTCCGTGCTGCAGTCGCTG
TTCAGCTCTGTGCCGGCCGCGCAGGCCTGGTGCACGTGTGCTCGTCCGCTGCCANACAGACTGACCAACTCGCACGCC
ATGGGCGAG

SEQ ID NO:314

>GL2_81A_D08_G3F1 Direction: N/A

CTGGACGGCCTGGCTGGGCTGAAGGGCGAGGACAGCCGAGCAAGGAGGCAGGGGAGGGCGGCCTACCGCTGTGCG
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GNCACAACCTCTTCATCTCTGCGGCGGCGTGCCTCCCGGAAGCCTCCTCAGCGGCCCCGGCCTGGCCCCGGCGGCG
TCCTCCGCGAGGCGGCGGCGTCTCCTCCGCCAGACGCACCGGTCTTCTTGGGCCCCCTTCCGCGGGGACCGCAG
TTCGCGCTCGGCCCATGTCCCTGCGAGGCCAACCTCGGCTCCGTGGCCGGCTCCTCCGTGCTGCAGTCGCTGTTCA
AGCTCTGTGCTGGCCTGCCGCGAGGCCTGGTGCACGTGTGCTCGTCCGCTGCCANACAGACTGACCAACTCGCACGCC
ATGGGCGAG

SEQ ID NO:315

>GL2_81A_D11_G3F1 Direction: N/A

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SEQ ID NO:316

>GL2_81A_D12_G3F1 Direction: sense

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SEQ ID NO:317

5 Clone 75 -Novel (KIAA1814)>

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SEQ ID NO:318

15 >gi|22053031|ref|XM_046822.3| Homo sapiens KIAA1814 protein (KIAA1814),
mRNA

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SEQ ID NO:319>gi|22053032|ref|XP_046822.3| similar to FLJ00192 protein [Homo sapiens]

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SEQ ID NO:320

Novel (maps to chromosome 4)

Novel (Chromosome 4) >

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SEQ ID NO:321

Novel peroxidase-like/ melanoma antigen

>GL2-86-4M13F Direction: sense

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SEQ ID NO:322

>GL2_93_2B08_G3F1 Direction: sense

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 45 GCACATCACCTACCAGCACTGGCTCCCGAAGATCCTGGGGGAGGTGGGCATGAGGACGCTGGGAGAGTACCACGG
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SEQ ID NO:323

Novel peroxidase-like/ melanoma antigen>

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SEQ ID NO:324

>gi|20533845|ref|XM_056455.2| Homo sapiens Melanoma associated gene (D2S448), mRNA

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5 GACTGCTGTGAAGACTGTAGGACCAGGGGGCAGTTCAATGCCTTTTCTATCATTTCCGAGGCAGACGGT
CTCTTGAGTTTCACTACCAGGAGGACAAGCCGACCAAGAAAACAAGACCACGGAAAAATACCCAGTGTGG
GAGACAGGGGGAACATCTCAGCAACAGCACCTCAGCCTTACAGACACGCTCAGATGCATCTGGGACAAAT
GACTTCAGAGAGTTTGTCTGGAATGCAGAAGACCATCAGACCTCAGAACACAGATAAAGAACTTG
10 AATCACGGCTCAGTACCACAGAGTGCCTGGATGCCGGGGGCGAATCTCACGCCAACACACCAAGTGGAA
AAAAGATGCATGCACCATTGTGAATGCAAAGACGGGCAGGTCACCTGCTTCGTGGAAGCTTGCCCCCT
GCCACCTGTGCTGTCCCCGTGAACATCCAGGGGCTGTGTCCAGTCTGCTTACAGAAGAGGGCGGAGG
AAAAGCCCTAGGCTCCTGGGAGGCTCCTCAGAGTTTGTCTGTGTGCCATCGTGAGATCGGGTGGCCGAT
15 GTGCTGTTACAGAAGGCAGTGCAGGAGGCTTCCAACAGAGCATCTGCGGAGAAGGAGGCACAGCAGTG
CCTGAAGGGAAGCAGGCAGGAGTCTAGCTTACGTTAGACTTCTCAGGTTTATTTAATTTCTTTTAAA
ATGAAAAATTGGTGCTACTATTAAATTGCACAGTTGAATCATTTAGGCGCTAAATTGATTTTGCTTCCC
AACACCATTCTTTTTTAAATAAAGCAGGATACCTCTATATGTCAGCCTTGCTTGTTCAGATGCCAGGAG
CCGGCAGACCTGTCACCCGAGGTGGGGTGAGTCTTGGAGCTGCCAGAGGGGCTCACCAGAAATCGGGGTT
20 CCATCACAAGCTATGTTTAAAAAGAAAATTGGTGTTTGGCAAACGGAACAGAACCTTTGATGAGAGCGTT
CACAGGGACACTGTCTGGGGGTGCAGTGCAAGCCCCCGGCTCTTCCCTGGGAACCTCTGAACCTCTCCT
TCCTCTGGGCTCTCTGTAACTTTTACCACACGTCAGCATCTAATCCCAAGACAAACATTCCCGCTGCTC
GAAGCAGCTGTATAGCTGTGACTCTCGTGCTCAGTCTTCCACACCTGATTAGAACATTCTAAGC
CACATTTAGAAACAGGTTTGTCTTTCAGTGTCTGTCACACATACTGCTTAGTTGTGAACCAATGTGA
25 AAAAACCTCCTTCATCCATTGTGTATCTGATACCTGCCGAGGGCCAAAGGGTGTGTGTGACAACGCCGC
TCCCAGCCGGCCCTGGTTGCGTCCACGTCTGAACAAGAGCCGCTTCCGGATGGCTCTTCCAAGGGAGG
AGGAGCTCAAGTGTGCGGAACCTGTCTAACTTCAAGTTGTGTGAGTGCGTTAAAAAAGGAGGAGGAGG
ATCCCTATACCTCATTTGTATTTTTTAAATGCGTGATGTTTATGAAATTGTGTCCATTTTTTAGGTATT
AGATATGGCAGAAAAACATTTCCACTATGCAAGTTCTTTTAGACGTCAGTGAAATCAACTCTCATAC
30 CTCATGGTCTCTCTTAAATTGACCAAAACCTTCCATTTTCTCTAAATACAAAGCGATCTGTGTTCTGAG
CAACCTTTCCCGGAACACACAGCTTCACTGTCAGCAGCCTGACCTGAGTATCCACCATGTGCCAGGCACAG
TGCTGGGCACACAGGCACCAAGGTCGCGGCCAGCTGCCCGCAGCAAGGCCAGCTGAGGTGGTGGAGGG
AGCCCCTGAGGTGAGGGGCCGTTTTCGGTTCAGGGTGCGAGGTGTCCAGCACTGGGGTATGGCGTCAAGGC
TTCCATGGGGTGGGGGAGGCCAGCTTCTTCTGACAGGATGGGCGCATACAGTGCCTGGTGTGATTGTG
35 CACAACCCGTGTTCCAGGTGCACATCTTCCAAGGAGACACCAGACCTTCCAGCACGGGCGGCCAAG
TTGCTGCGGCGGAGGCAGCATTTCAGCTGTGAGGAAGGTCAATTGGATTATGTGTTTTATCTGTAAAAAT
GGTGTCTTAACTTCTTAACTCATATTGTAAGTGATGATAAAAAATTGGTTGGTGTTCATGACATGT
GGACTTCTTTTGAATAGCAAGTCAAAATGTAGTGACCAAAATTGTGGAAGAGATTCTGTCAAATAGGAAA
40 TGTGTAAGTTCTGCTAAAAGCTGATGGTTATGTAAGTTGCTCAGGCACCTCAGATGACAGCAGATTCTGGG
TTCTGGGAGTGTTCTGTGCTCTTACATGCCCTGGAGGCCCTCATGGTCTCAGTGTGAGGCGGCACACCT
GTAGCACACCTGCGTAATGTGCGGTCTGGGCGAGTGCACAAAGGAATTGTGTTGTCTAAGCCAAAGGGGAA
GCTGACTGTGATTTACCAAAAAAATTCTGTAATTCAAACCAAAATGTCTGCGGAATCACCAGGTGATA
CTCTCTGTAATCAGAACAGTGGGCAGTGCTGGGTGAACGTGTCTAGCAGCCACTGTGCGGGATCGCTGT
AACAGGAGTGAATGTACATATTTATTTACTTTTCTAACTGCTCCAACAGCCAAATGCCTTTTTTATGAC
45 CATGTATTACAGTTCATTACCAAGAAATGTTTGCACTTTGTAATGATGCCTTTCAGTTCAAATAAATGG
GTCACATTTTCAAATGG

SEQ ID NO:325

50 >gi|20533846|ref|XP_056455.2| similar to Peroxidasin [Homo sapiens]
MAKRSRGPGRRLALVLFCAWGTAVVAQKPGAGCPSRCLCFRTTVRCMHLLLEAVPAVAPQTSILDLR
FNRIREIQPGAFFRLRLNLTLLNNNQIKRIPSGAFEDLENLKYLYLYKNEIQSIDRQAFKGLASLEQLY
LHFNQIETLDPDSFQHLPLKLERLFLHNNRITHLVPGTFLHLESMKRLRLDSNTLHCDCEILWLADLLKTY
AESGNAQAAAI CEYPRRIQGRSVATITPEELNCERPRITSEPQDADVTSGNTVYFTCRAEGNPKPEIIWL
RNNNELSMKTD SRLNLDDGTLMIQNTQETDQGIYQCMKNVAGEVKTQEVTLRYFGSPARPTFVIQPN
55 TEVLVGESVTLCSATGHPPPRI SWTRGDRTPLPVDPRVNITPSGGLYIQNVVQGDSEYACSATNNIDS
VHATAFIIVQALPQFTVTPQDRVVEGQTVDFQCEAKGNPPVIAWTKGGSQLSVDRRLVLSSTGLRIS
GVALHDQGYEQAVNIIGSQKVVHLTVQPRVTPVFASIPSDTTVEVGANVQLPCSSQGEPEPAITWNK
DGVQVTESGKFHISPEGFLTINDVGPADAGRYECVARNITGSASVSMVLSVNVPDVSRRNDPFFVATSIVE
AIATVDRAINSTRHLEFDRSPNDLLALFRYPDPYTVQARAGEIFERTLQLIQEHVQHGLMVDLNG
60 TSYHYNDLVSPQYLNLIANLSGCTAHRVNNCSDMCFHQBKRYRTHDGTNNLQHPMWGASLTAFERLLKSV
YENGFNTPRGINPHRLYNHALPMPRLVSTTLIGTETVTPDEQFTHMLMQWGQFLDHDLDSTVVALSQR
FSDGQHCSNVCSNDPPCF SVMIPPND SRARS GARC MFVRSSPVC GSGMTSLLMNSVYPREQINQLTSYI
DASNVYGSTEHARSIRDLASHRGLLRQGI VQRSGKPLLPFATGPPTCEMRDENESPIPCFLAGDHRANE
QLGLTSMHTLWFREHNRIATELLKLNPHWDGDTIYYETR KIVGAEIQHITYQHWLPKILGEVGMRTLGEY
65 HGYDPGINAGIFNAFATAAFRFGHTLVNPLLYRLDENFQPIAQDHLPLHKAFSPFRIVNEGGIDPLLRG
LFGVAGKMRVPSQLNTELTERLFSMAHTVALDLAAINIQRGRDHGIPPYHDYRVYCNLSAAHTFEDLKN

BIKNPEIREKLKRLYGSTLNIDLPALVVEDLVPGSRLGPTLMCLLSTQFKRLRDGDRWLWYENPGVFSFA
QLTQIKQTSRLARILCDNADNITRVQSDVFRVAEFPFHGYGSCDEIPRVDLRVWQDCCEDCRTRGQFNFSY
HFRGRSLEFSYQEDKPTKKTRPKIPSVGRQGEHLSNSTSAFSTRSDASGTNDFREFVLEMQKTTIDLR
TQIKKLESRLSTTECVDAGGESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNI PGACCPVC
LQKRAEEKP

SEQ ID NO:326

Novel WD40/SOCS box protein

>GL2_81_2_M13F Direction: anti-sense

GGCTTGACCTTGCCACGGTGGCAGATGACAGACTCCTCAGGATCTGGGCCCTGGAAC TGAAACTCCCAGTTGC
ATATTGCATCCTATNACCAATGGGCTTTGCTGCACATTTTTTCCACATGGTGGAGTCATTGCCACAGGGACAAGA
GATGGCCACNTCCAGTTCTGGACAGCTCCTAGGGTCTGTCTCTCACTGAAGGCACTTATGCCGGAAGCCCTTCG
AAGTTTCTAACAACCTTACCAAGTCTAGCACTGCCTATCCCCAAGAAAATGAAAGAGTTCTCTACATACAGGAC
TTTTGTAAAGCAACACCAGCATCTTGTGCTTCTTTGGTGAGCAGGTAAATCGTCTGTCAAGGGAGTTGCTGGAA
TAATGGGCCAAACATCTGGTCTTGCATTGAAATAGCACTTTCTTTGGGATTGTGAATAGAATGTAGCAAAACCAG
ATTCCAGTGTACTAGTCATGGATCTTTCTCTCCCTGGCATGTGAAAGTCAGCTTAGAGGAAGAGATCCACTTGCA
CCGGCAGAGCCGCGGAGAACCAGCGACACTGGGAGCACGGTGGCAACGGCCCTGGCGGCTCTCTGTACAGCT
CGTCANGCCGAGAGAAGGCCAAAATNCGGGAACCTGATGGAATCGCCCTTAGTGAGGGTATCCAGAACTGGCAA
CATGCCANAAACGGTACCGGGTAAACTGTTCCCCCATCCCCAAAAAACCNACAAAGGACCGGCCNCACATAA
CAACACACAAAAGCGCACANCCATCACAGA

SEQ ID NO:327

>GL2_81_3_M13R Direction: anti-sense

GGCTTGACCTTGCCACGGTGGCAGATGACAGACTCCTCAGGATCTGGGCCCTGGAAC TGAAACTCCCATTGCA
TTTGCTCCTATGACCAATGGGCTTTGCTGCACATTTTTTCCACATGGTGGAGTCATTGCCACAGGGACAAGAGAT
GGCCACGTCCAGTTCTGGACAGCTCCTAGGGTCTGTCTCTCACTGAAGCACTTATGCCGGAAGCCCTTCGAAGT
TTCCTAACAACCTTACCAAGTCTAGCACTGCCAATCCCCAAGAAAATGAAAGAGTTCTCTACATACAGGACTTTT
TTAAGCAACACCACATCTTGTGCTTCTTTGTAG

SEQ ID NO:328

>GL2_81_2_M13R Direction: sense

CGGNTCTGTTGCCGTGCAAGTGGAATCATCTTACCTCTAAGACATGACTTTTACATGCCAGGGGAGAGAAAGATC
CATGACTAGTACACTGGCAATCTGGTTTTGCTTACATTCTATTACAAATCCCNAAAGAAATGCTATTTCAATGCAAG
ACCAGATGTTTGGCCCATTTATCCAGCAACTCCCTTTGACAGGACGATTTACCCTGCTACAACAGAAGCACACAG
ATGTGGTGTGCTTAAAAAAGTCTGTACTGTGAGGAACTCTTTCACTTTTCTTGGGGATTGGCCACGTGCTATG
GACTTAGGTAAGTTGTTTCAAGAACTTCGCAAGGGCTTTCCGGCATAAGTGCTATCAGTGAGGACAGGACCCTAG
TGAGCTGTCCAGAACTGGACGTGGCCATCTCTTGTCCCTGTGGCCAATGACTCCACCATGTGGAATACATGTNCA
GCAAAGCCCATTTGGTCATAAGAAACAAAATGCAATCGGGAGTTNCCAGGTCCAGGGGCCCCGAGATCCTGAGGGAGG
TCNTGTGCAATCTGCCAGCGTGGCAAGGGTACCAAGCCCCGANAAAACCCAGAGCAACAAGGTGGGTCTCAGA
ATNAGAATCAAGCGGGCCGGTCCGANACTAGCCCTTCGAGGGGTCTTGAAATACTCACCAAAGGNGCGCAAATA
AGGGGGGCGACATCTCGTTTCAAAACCTCGCCGAAAAAGACNCCTAGGATGAANGGCTACAAATGACCAGCGTGA
GAAACACTGGCCNCGCAGACCCCGGGGTGAC

SEQ ID NO:329

Novel WD40/SOCS box protein>

CGGCTCTGTTGCCGTGCAAGTGGAATCATCTTACCTCTAAGACATGACTTTTACATGCCAGGGGAGAGAAAGATC
CATGACTAGTACACTGGCAATCTGGTTTTGCTTACATTCTATTACAAATCCCAAAGAAATGCTATTTCAATGCAAG
ACCAGATGTTTGGCCCATTTATCCAGCAACTCCCTTTGACAGGACGATTTACCCTGCTACCAAAGAAGCACAGA
TGTGGTGTGCTTAAAAAAGTCTGTATGTGAGGAACTCTTTCACTTTTCTTGGGGATTGGCAGTGCTAGGACTTG
GTAAGTTGTTAGGAACTTCGAAGGGCTTTCCGGCATAAGTGCTTCACTGAGGACAGGACCCTAGGAGCTGTCCA
GAAC TGGACGTGGCCATCTCTTGTCCCTGTGGCAATGACTCCACCATGTGGAATAATGTGCAGCAAAGCCCAT
GGTCATAGGAGCAAATGCAATGGGAGTTTTTCACTTCCAGGGCCAGATCCTGAGGAGTCTGTCTATCTGCCACCGT
GGCAAGGTACAAGCCCCCG

SEQ ID NO:330

>gi|20149658|ref|NM_018639.2| Homo sapiens CS box-containing WD protein (LOC55884), mRNA

CGGACGCGTGGGGCCCGGGGGCTGAGGCGCCCCGCCGCTGCCGCGGGGGCCGCTCGCGTCTCTCCATGGA
GGCCGGAGAGGAACCGCTGCTGCTGGCCGAACCAAGCCCGGGCGCCCCACCAGTTTGATTGGAAGTCC
AGCTGTGAAACCTGGAGCGTCGCCTTCTCCCCAGATGGCTCCTGGTTTGCTTGGTCTCAAGGACACTGCA

TCGTCAAACCTGATCCCCTGGCCGTTGGAGGAGCAGTTTCATCCCTAAAGGGTTTGAAGCCAAAAGCCGAAG
TAGCAAAAATGAGACGAAAGGGCGGGGAGCCCAAAAGAGAAGACGCTGGACTGTGGTCAGATTGTCTGG
GGGCTGGCCTTCAGCCCGTGGCCTTCCCCACCCAGCAGGAAGCTCTGGGCACGCCACCACCCCAAGTGC
5 CCGATGTCTCTTGCCTGGTTCTTGCTACGGGACTCAACGATGGGCAGATCAAGATCTGGGAGGTGCAGAC
AGGGCTCCTGCTTTTGAATCTTTCCGGCCACCAAGATGTCGTGAGAGATCTGAGCTTCACACCCAGTGGC
AGTTTGATTTTGGTCTCCGCGTCACGGGATAAGACTCTTCGCATCTGGGACCTGAATAAACACGGTAAAC
AGATTCAGTGTTATCGGGCCACCTGCAGTGGGTTTACTGCTGTTCCATCTCCCCAGACTGCAGCATGCT
GTGCTCTGCAGCTGGAGAGAAGTCGGTCTTTCTATGGAGCATGAGGTCTACACGTTAATTCGGAAGCTA
10 GAGGGCCATCAAAGCAGTGTTGTCTCTTGTGACTTCTCCCCGACTCTGCCCTGCTTGTACGGCTTCTT
ACGATACCAATGTGATTATGTGGGACCCCTACACCGGCGAAAGGCTGAGGTCACTCCACCACACCCAGGT
TGACCCCGCCATGGATGACAGTGACGTCCACATTAGCTCACTGAGATCTGTGTGCTTCTCTCCAGAAGGC
TTGTACCTTGCCACGGTGGCAGATGACAGACTCCTCAGGATCTGGGCGCTGGAACCTGAAAACCTCCATTG
CATTTGCTCCTATGACCAATGGGCTTTGCTGCACATTTTTCACATGGTGGAGTCATTGCCACAGGGAC
AAGAGATGGCCACGTCCAGTTCTGGACAGCTCCTAGGGTCTGTCTCACTGAAGCACTTATGCCGGAAA
15 GCCCTTCGAAGTTTCTAACAACCTTACCAAGTCTTAGCACTGCCAATCCCCAAGAAAATGAAAGAGTTCC
TCACATACAGGACTTTTAAAGCAACACCACATCTTGTGCTTCTTTGTAGCAGGGTAAATCGTCTGTCAA
AGGGAGTTGCTGGAATAATGGGCCAAACATCTGGTCTTGCATTGAAATAGCATTTCTTTGGGATTGTGAA
TAGAATGTAGCAAAACAGGATTCAGTGTAAGTCTTCTCTCCCTGGCATGTGAAAGTCAG
TCTTAGAGGAAGAGATTCCACTTGACGGCAACAGAGCCTTACGTTAAATTTTCAGTCCAGTTATGAACA
20 GCAAGTGTTGAACTCTTCTGCTTGTGTTTATTGATTCAAAGTGCAGTTACTGATGTTGTTTTGATTATGCAAC
TAAGTAGGCCTCCAGAGCCTCTCTAGTGGCAGAGCAGCTCACACTCCCTCCGCTGGGAACGATGGCTTCT
GCCTAGTACCTATCCTTGTGTTTCTGATGCAGTGGTAGCATTGGTTCAAGTTCTCTCCTGCTGTGGTCAG
AGTTGCTTCGATGTTGGCCAAGTGCTTTTCTTCTGGGCTCCCTTCTGACCTGCAGGACAGTTTTCCTGG
AGCCATTTGGTATGAGGTATTAATTTAGCTTAACTAAATTACAGGGGACTCAGAGGCCGTGCTCCTGACC
25 GATCCAGACACTATTACTGGCTTTTTTTTTTTTTTAAACATGGTGTGCATGTGCAGGAAATGACAAATTT
GTATGTCAGATTATACAAGGATGTATTCTTAAACCGCATGACTATTGAGTGGCTACTGAGTTATCAGTG
GCCATTTATTAGCATCATATTTATTTGTATTTTCTCAACAGATGTTAAGGTACAACGTGTGTTTTCTCGA
TTATCTAAAAACCATAGTACTTAAATTGAACAGTTGCAAGATGTCTTAATTGTGTAAAGAATTGGTGTA
GTGATGACTTTAGCTGATACTCTTATGTACGAGATCTGTCTCTGCTGTTTAACTTCATTGGATTAATCAG
30 CTGGTTTCAACTCTACTGCGAAACAAAATAGCTCCTTAAAGTACTGTTCTCCTTCAGTGGCATGTAGT
TATCTAATCAAGACACCTCATTCAAACAAAACCTGCCTTAGGAAAATTTAATATATTTTAAATTATTTTA
AAAGAAATACAACATCTTATTCTTTAGCTTTCTTAATCGGTGCTTTATGGAGGCCAGTGTAAACGTTACAT
GACTCGTTGAGAAAGTTGAGGAATTTCTCTACCACCTTTGTTGCTTGAAGAAAAACATGTCTTTTCAA
ATGAGAGGCTTTCATTGAAGAAAAAGAAAAAAACAACAGTTAAAAAAGAAAAAAGAAAAAAGAAAAA
35 AAAAAAAGAAAAAAGAAAAA

SEQ ID NO:331

>gi|8923881|ref|NP_061109.1| CS box-containing WD protein [Homo sapiens]
MEAGEEPLLLAELKPRPHQFDWKSSCETWSVAFSPDGSWFAWSQGHCIIVKLIPWPLEEQFIPKGFCAKS
40 RSSKNETKGRGSPKEKTLDCGQIVWGLAFSPWPSPSRKLWARHHPQVPDVSLVLATGLNDGQIKIWEV
QTGLLLNLSGHQDVVRDLSTFPGSLILVSASRDKTLRIWDLNKHGKQIQVLSGHLQWVYCCSISPDCS
MLCSAAGEKSVFLWSMRSYTLIRKLEGHQSSVVSDFSPDSALLVTASYDNTNIMWDPYTGERLRLSLHHT
QVDPAMDDSDVHISLRSVCFSPGELYLATVADDRLLRIWALELKTPIAFAPMTNGLCCTFFPHGGVIAT
45 GTRDGHVQFWTAPRVLSSLKHLCKALRSFLTTYQVLALPIPKMKKEFLTYRTF

SEQ ID NO:332

Numb-like

>GL3_16A_3 M13R Direction: anti-sense

CGTCTGCCCTGCCACTGGTGCAGGGCGCGACGCCTCGGGCAGCTAGGCTGGCTTCTCCGCCGAGGGCTCTTGNCC
50 GGTAAAACCTTGTTCATGGTGCCCGCACCCGCTCTGGCTCCGTCCTGCAGGGTTTCTTGGGGGGCCCCGGGGCCCC
CACAAGGGGGACTGGGGGGCAGGGTGCCGGTTCAAGGGCCCCCTTCTTTGTTACAGGCTTCGGTCCAATGCNG
AGAAGGAAAGGGGCGAAATTCNCTGCAGAATA

SEQ ID NO:333

>GL3_16A_4 M13R Direction: anti-sense

CGTCTGCCCTGCCACTGGTGCAGGGCGCGACGCCTCGGGCAGCTAGGCTGGCTTCTCCGCCGAGGGCTCTGCCGTA
ACTTGTTCATGGTTGCCCCGCCCCGCTCTGGCTCCGCTCCTGCAGGTTTCTGGAGGCCACCGTTGCCATCGGGCCTAT
GGGCGGGCCTTCTTCTCCCTTTGTTACCAGGCCTTCCGGTTCCCAATAGCCCCGGAAGGAAGAAAACGGGGGCGG
AAATTTCTTGGCCAGGAGTTATTTCCCNATTTCAAACAACTTGGGCCGGGGGACCCGGAGTTTCCGGAAGCNC
60 ATATTTGNCAAATTTTATAAGGAGAAGGGGGGGGGCCCCACAAAATTTTTCGGCAGCCCCCTTAAATTTANGGT

TTGAGAAAGGATTTCCGGTAATTTTACACCAAATTTTCAACTTTGTGGGGCGCCAGGATACAGAGGATAT
 TAAAAACACAAAAACGGCGGGGTANCAGGGGTNTGGGGNCCTTTGGGGGGGAGAGAAGAAAAACCCGCCCCCT
 TTTTGTGGGCGCGNGNTTTTATAACGCCCCCCCCGANAAAATCCTTTTATAAAATTTTCATGCGAGCCGCCGTT
 TTTTNTGGNGTGAGAGAGGGACAGGAGCACAAATATTTTCCCCCGCCCTNTTTATTTTACCGAGGGCG
 5 CCCCANAGGCGTTATTGGGGACGCGGCCGTTTACAAAATAATAATGACGCTGCGAGAAAAATAGAGAAAAG
 GGTGCCCCCCCCCTGCGGAGAANAACCCCGCGGNGNAGATATTACTTGGCAGGGAGCGCCCTTTTAT

SEQ ID NO:334

>GL3_39L_1_M13R Direction: anti-sense

CGTCTGCCCTGCCACTGGTGCGGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGAGGCTCTGCCGTA
 ACTTGTTCATGGTGCCCGCCCCGCTCTGGCTCCGTCTGCAGGTTTCTGGGGGCCCCGGGGCCCCAACAGGG
 GGGCCTTGGGGGGGCGAGGTTGCCGAGAAGCCCAAGGCAACACTTGGNGAAAGCCCAACCGNTAGGCACAA
 CCGGGGCCACTTATNGGCGANGGAGCCATNACACATTCCCTTTTGGTTACCCAAGGGCANATCCGGATCCCCAAT
 TTGCACCCGGANATGGAAGCAAAAGGGGGCGCGGAAAAATTTCTTTGCCCGAGGATTAATTTCCCCAAATT
 15 CCAAACACACCCTGTGGTGGCAGGGNGACCACGGAATTCCGAAAAGGCCNATTTTGGCCCATATTCTTTTAGGG
 AAAGGGGGGGCCCCCCCCAAAAGAATTTTGTTCNNGCCCCCATATATAAA

SEQ ID NO:335

>GL3_16A_2_M13R Direction: anti-sense

CGTCTGCCCTGCCACTGGTGCGTGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGAGGCTCTGCCGT
 TAAACTTGTTTCATTTGGTGCCCGCCCCGTTCTTGGCCTCCGTCCCTTGCAGGTTTCTGGGGGCCCCGGNNGGGGCC
 CCAAACAGGGGGTGGCTTTGGAAGCCCCCAACCGGGTTGCCAACNCGGACACTATGGGGGACCTTTACATTCC
 TTTTGTACCAGGCTTCGGTTTACAATTGGCCCCGAAGGAAAGAAAAGGGGCGCGGAAATTTCTTGTGCCAAGG
 ATTTTATTCCCAATTTTCAAGCGACCGTTGGGCCGGGGACCCCGACTCCGAAGCCATTTGGCAATTCATNAG
 25 GGAAAGGGNGCCCCCAAATTTTCGCGGACCCTATAAATAAGATTGAGCAGACTCGGGTAATTTATAACAAATTT
 TACCACAACGCGTTGTGGGGACCCCCGGGTATACTGCAGGTTATTTATTATAACCANAAAAGGCGGTGATATTC
 CANGTAGTTGTGGAACCTGTGTGGNGGGGAAACAAAAAAAACACACCCCCCCCCCTTTTGGGGTANGGC
 CGGGTGATTTTATAACAACCCCCCAGCCAAAAAGAACCGCTTTTNTAANAAG

SEQ ID NO:336

>GL3_39L_3_M13F Direction: N/A

CGAGGAGGCTCGCGCGCGTGCATCCCGCACCATCCCCAGCCCCAGAAACCTGCAGGACGGAGCCAGACGGGGT
 GGGCACCATGAACAAGTTACGGCAGAGCCTGCGGCGGAGGAAGCCAGCCTACGTGCCCCAGGGCCGTGCGCCCCG
 AACCAGTGGCAGGCAGACG

SEQ ID NO:337

>GL3_39L_3_M13R Direction: anti-sense

CGTCTGCCCTGCCACTGGTGCGGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGAGGCTCTGCCGGT
 AACTTGTTCATGGTGCCACCCCGTCTGGCTCCGTCTGCAGGTTTCTGGGGGCTGGGGGATGGTGCGGGATGCA
 40 ACGCGCGCGAGCTTCCTCG

SEQ ID NO:338

>GL3_16A_1_M13F Direction: anti-sense

CGTCTGCCCTGCCACTGGTGCGGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGAGGCTCTGCCGTA
 45 ACTTGTTCATGGTGCCCGCCCCGCTCTGGCTCCGTCTGCAGGTTTCTGGGGGATGGTGCGGGATGCACGCGCGCG
 AGCCTCCTCG

SEQ ID NO:339

>GL3_16A_1_M13R Direction: sense

CGAGGAGGCTCGCGCGCGTGCATCCCGNACCATCCCCAGAAACCTGCAGGACGGAGCCAGACGGGGCGGGCACC
 50 ATGAACAAGTTACGGCAGAGCCTGCGGCGGAGGAAGCCAGCCTACGTGCCCCAGGCGTGCGCCCGACCAAGTGGC
 AGGCAGACG

SEQ ID NO:340

>gi|10863898|ref|NM_004756.1| Homo sapiens numb homolog (Drosophila)-like
 (NUMBL), mRNA

ATGTCCCGCAGCGCGGGCCAGCGGCGGACCCCGAGGCCTGAGCGGCACCTGCCCCCAGCCCCCTGTG
 GGGCCCCGGGGCCCCCAGAAACCTGCAGGACGGAGCCAGACGGGGCGGGCACCATGAACAAGTTACGGCA
 GAGCCTGCGGCGGAGGAAGCCAGCCTACGTGCCCCAGGCGTGCGCCCGCACCAGTGGCAGGCAGACGAG
 60 GACGCGGTGCGGAAGGGCACGTGCAGCTTCCCGGTGAGTACCTGGGTACGTGGAGGTAGAGGAGTCCC

GGGGAATGCACGTGTGTGAAGATGCGGTGAAGAAGCTGAAGGCGATGGGCCGAAAGTCCGTGAAGTCTGT
CCTGTGGGTGTCAGCCGATGGGCTCCGAGTGGTGGACGACAAAACCAAGGATCTTCTGGTCCGACCAGACC
ATCGAAAAGGTCTCCTTTTGTGCTCCTGACCGCAACCTGGACAAGGCTTTCTCCTATATCTGTCTGTGACG
5 GGAATACCCGCCGCTGGATCTGCCACTGTTTTCTGGCACTGAAGGACTCCGGCGAGAGGCTGAGCCACGC
TGTGGGCTGTGCTTTTGGCGCTGCCTGGAGCGAAAACAGCGACGGGAGAAGGAATGTGGGGTACGGCC
GCCTTTCGATGCCAGCCGCACCAGCTTCGCCCCGCGAGGGCTCCTTCCGCCTGTCTGGGGGTGGGCGGCCTG
CTGAGCGAGAGGCCCCGGACAAGAAGAAAGCAGAGGCAGCAGCTGCCCCCACTGTGGCTCCTGGCCCTGC
CCAGCCTGGGCACGTGTCCCCGACACCAGCCACCACATCCCCCTGGTGAGAAGGGTGAGGCAGGCACCCCT
10 GTGGCTGCAGGCACCACTGCGGCGGCCATCCCCGGCGGCCATGCACCCCTGGAGCAGCTGGTTCCGCCAGG
GCTCCTTCCGTGGGTTCACGACTCAGCCAGAAGAACTCGCCTTTCAAACGGCAGCTGAGCCTACGGCT
GAATGAGCTGCCATCCACGCTGCAGCGCCGCACTGACTTCCAGGTGAAGGGCACAGTGCCCTGAGATGGAG
CCTCCTGGTGCCGGCGACAGTGACAGCATCAACGCTCTGTGCACACAGATCAGTTCATCTTTTGGCAGTG
CTGGAGCGCCAGCACCAGGGCCACCACCTGCCACAACAGGGACTTCTGCCTGGGGTGAGCCCTCCGTGCC
CCCTGCAGCTGCCCTTCCAGCCTGGGCACAAGCGGACACCTTCAGAGGCTGAGCGATGGCTGGAGGAGGTG
15 TCACAGGTGGCCAAGGCCAGCAGCAGCAGCAGCAACAGCAACAGCAGCAGCAGCAGCAGCAAC
AGCAGCAAGCAGCCTCAGTGGCCCCAGTGGCCACCATGCCTCCTGCCCTGCAGCCTTTCCCCGCCCCCGT
GGGGCCCTTTGACGCTGCACCTGCCCAAGTGGCCGTGTTCTGCCACCCCCACACATGCAGCCCCCTTTT
GTGCCCGCTACCCGGGCTTGGGCTACCCACCGATGCCCCGGGTGCCCCGTGGTGGGCATCACACCCCTCAC
AGATGGTGGCAAACGCCTTCTGCTCAGCCGCGCCAGCTCCAGCCTCAGCCTGCCACTCTGCTTGGGAAAGC
20 TGGGGCCTTCCCCGCCCCCTGCCATACCCAGTGGCCCTGGGAGCCAGGCCCGCCCTCGCCCCAATGGGGCC
CCCTGGCCCCCTGAGCCAGCGCCTGCCCCAGCTCCAGAGTTGGACCCCTTTGAGGCCCAAGTGGCGGCAT
TAGAAGGCAAAGCCACTGTAGAGAAACCCTCCAACCCCTTTTCTGGTGACCTGCAAAAAGACATTTCGAGAT
TGAAGTGTAG

25 SEQ ID NO:341

>gi|10863899|ref|NP_004747.1| numb homolog (Drosophila)-like; numb
(Drosophila) homolog-like [Homo sapiens]
MSRSAASGGPRRPERHLPPAPCGAGPPETCRTEPDGAGTMNKLRLRRRKPAYVPEASRPHQWQADE
DAVRKGTCSFPVRYLGHVEVEESRGMHVCEDAVKKLKAMGRKSVKSVLWVSADGLRVVDDKTKDLLVDQT
30 IEKVFSFAPDRNLDKAFSYICRDGTTTRRWICHFLALKDSGERLSHAVGCAFAACLERKQREKECGVTA
AFDASRTSFAREGSFRLSGGGRPAEREAPDKKKAEEAAAPTVAEPGAQPGHVSPTPATTSPEGKEGAGTP
VAAGTTAAAIPIRRHAPLEQLVRQGSFRGFPALSQKNSPFRQLSLRLNELPSTLQRRITDFQVKGTVPME
PPGAGSDSINALCTQISSSFASAGAPAPGPPPATTTGTSANGEPSVPPAAAFQPGHKRTPSEAERWLEEV
SQVAKAQQQQQQQQQQQQQQQAASVAPVPTMPALQFPAPVGPFDAAAPAQVAVFLPPPHMQPPF
35 VPAYPGLGYPPMPRVVVGITPSQMVANAFCSAAQLQPPATLLGKAGAFPPPAIPSAQSGARPRPNGA
PWPPEPAPAPAPELDPFEAQWAALEGKATVEKPSNPFSGDLQKTFEIEL

SEQ ID NO:342

P130Cas (Crk-associated substrate)
>GL1_43_2_1_M13F Direction: sense
40 CGCGGGATGTCTACTCGTCTCCTGCTCCGGCTGGGCGGCCTCGTATACATAGCCCTGCCCCACGCGGTGGGCACC
ACCACCTTTGCCGGGGCTTCGTGCCCTCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTCATGC
CCCATCCCCGAGAAAGGTGGCACCTGGTAAATATCTTGGGCAGGGCTCCAGGCCCTGGGGGCACCTGGTACAGG
TCTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC
45

SEQ ID NO:343

>GL1_43_2_1_M13R Direction: anti-sense
GCCAAGCAGACATCCACCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCGCCACAGACCTGTACCAG
GTGCCCCCAGGGCCTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACATC
50 TACCAGGTCCCCCGATCCATGGACACACGCAGCTGGGAGGGCACGAAGCCCCGGCAAAGGTGGTGGTGGCCAC
CCGCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCGCG

SEQ ID NO:344

>GL1_43_3_6_M13F Direction: sense
55 CGCGGGATGTCTACTCGTCTCCTGCTCCGGCTGGGCGGCCTCGNTATACATAGCCCTGCCCCACGCGGTGGGCAC
CACCACCTTTGCCGGGGGCTTCGTGCCCTCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTCATG
CCCCATCCCCGAGAAAGTGGCACCTGGTAAATATCTTGGGCAGGGCCTCCAGGCCCTGGGGGCACCTGGTACAG
GTCTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC

SEQ ID NO:345

>GL1_43_3_6_M13R Direction: anti-sense

GCCAAGCAGACATCCACCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCCGCCACAGACCTGTACCAG
GTGCCCCCAGGGGCTTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACAT
5 CTACCAGGTCCCCCGTCCATGGACACACGCAGCTGGGAGGGCAGCAAGCCCCCGCAAAGGTGGTGGTGCCAC
CCGCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCGCG

SEQ ID NO:346

>GL1_43_4_4_M13F Direction: sense

CGCGGGATGTCTACTCGTCCTGCTCCGGCTGGGCGGCCTCGTATACATAGCCCTGCCCCACGCGGGTGGGCACC
ACCACCTTTGCCGGGGGCTTCGTGCCCTCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTCATGC
10 CCCATCCCGGCAGAAAGGTGGCACCTGGTAAATATCCTGGGCAGGGCCTCCAGGCCCTGGGGGCACCTGGTACAGG
TCTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC

SEQ ID NO:347

>GL1_43_4_4_M13R Direction: anti-sense

GCCAAGCAGACATCCACCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCCGCCACAGACCTGTACCAG
GTGCCCCCAGGGACCTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACAT
20 CTACCAGGTCCCCCGATCCATGGACACACGCAGCTGGGAGGGCAGCAAGCCCCCGCAAAGGTGGTGGTGCCCA
CCCGCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCGCG

SEQ ID NO:348

>GL1_43_4_6_M13F Direction: sense

CGCGGGATGTCTACTCGTCCTGCTCCGGCTGGGCGGCCTCGTATACATAGCCCTGCCCCACGCGGGTGGGCACC
25 ACCACCTTTGCCGGGGGCTTCGTGCCCTCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTCATGC
CCCATCCCGGCAGAAAGGTGGCACCTGGTAAATATCCTGGGCAGGGCCTCCAGGCCCTGGGGGCACCTGGTACAGG
TCTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC

SEQ ID NO:349

>GL1_43_4_6_M13R Direction: anti-sense

GCCAAGCAGACATCCACCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCCGCCACAGACCTGTACCAG
GTGCCCCCAGGGNCTTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACAT
30 CTACCAGGTCCCCCGATCCATGGACACACGCAGCTGGGAGGGCAGCAAGCCCCCGCAAAGGTGGTGGTGCCCA
CCCGCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCGCG

SEQ ID NO:350

>GL1_43_LOW_3_G3F1 Direction: sense

GCGGGATGTCTACTCGTCCTGCTCCGGCTGGGCGGCCTCGTATACATAGCCCTGCCCCACGCGGGTGGGCACCA
40 CCACCTTTGCCGGGGGCTTCGTGCCCTCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTCATGCC
CCATCCCGGCAGAAAGGTGGCACCTGGTAAATATCCTGGGCAGGGCCTCCAGGCCCTGGGGGCACCTGGTACAGGT
CTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC

SEQ ID NO:351

>gi|7656923|ref|NM_014567.1| Homo sapiens breast cancer anti-estrogen
45 resistance 1 (BCAR1), mRNA

GAGGCGGCAGCTGCGCGGCGGCACCGGGGCGGCTGCGGCGCGCTCGGAGCCCCGAGGCACGCGGCCCGGG
CAGCTCGGTGTGCGCCCCGCGAGAGCCGGGCCCCAGGCCCGCCGGACACCATGAACCACCTGAACGTGC
TGGCCAAAGCGTCTATGACAATGTGGCCGAGTCCCCGGATGAGCTCTCCTTCCGCAAGGGTGACATCAT
50 GACGGTGTGGAGCAGGACACGCAGGGCCTGGACGGCTGGTGGCTCTGCTCGCTGCATGGGCGCCAGGGC
ATCGTGCTGGGAACCGCTCAAGATCTTGGTGGGCATGTATGATAAGAAGCCAGCAGGGCCTGGCTCCG
GCCCTCCCGCCACCCCGGCCAGCCTCAGCCTGGCCTCCATGCCCCAGCGCCTCCGGCCTCCAGTACAC
GCCCCATGCTCCCCAACACCTACCAGCCCCAGCCAGACAGCGTCTACCTGGTGGCCACTCCCAGCAAGGCT
CAGCAAGGCCTCTACCAAGTCCCGGGTCCCAGCCCTCAGTTCCAGTCTCCCCCAGCCAAGCAGACATCCA
55 CCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCCGCCACAGACCTGTACCAGGTGCCCCCAGG
GCCTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACATCTACCAG
GTCCCCCGTCCATGGACACACGCAGCTGGGAGGGCAGCAAGCCCCCGCAAAGGTGGTGGTGCCACCC
GCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCGCGACACCT
GCTGGCCCCGGGGCCACAGGACATCTATGATGTGCCCCCGGTTCCGGGGGCTGCTTCCCAGCCAGTATGGC
CAGGAGGTGTATGACACACCCCCCATGGCTGTCAAGGGTCCCAATGGCCGAGACCCGTTGCTGGAGGTGT
60 ATGACGTGCCCCCAGTGTGGAGAAGGGCCTGCCACCGTCCAACCACCACGAGTCTACGACGTTCTCTCC

ATCGGTGAGCAAGGATGTGCCCCGATGGCCCACTGCTGCGTGAGGAGACCTACGATGTGCCCCCGCCTTC
GCCAAGGCCAAGCCCTTTGACCCGGCCCCGACCCCACTGGTACTGGCTGCGCCCCCTCCAGACTCCCCGC
CGGCCGAGGACGTGTATGACGTGCCGCCCGGCTCCTGACCTCTACGACGTGCCCCCTGGCTTGCGGCG
5 GTGGTGCAGAGTGGTGTGTATGCGGTGCCTCCCCAGCTGAACGTGAAGCCCCGGCAGAGGGCAAGCGCC
TGTCGGCCTCCAGCACCGGCAGCACACGAGCAGCCAGTCTGCGTCTCTTGGAGGTGGCAGGGCCGGG
CCGGGAACCCCTGGAGCTGGAAGTTGCTGTGGAGGCCCTGGCACGGCTGCAGCAGGGTGTGAGCGCCACC
GTTGCCACCTTCTGGACCTGGCAGGCAGCGCCGGTGCAGTGGGAGCTGGCGTAGCCCCCTCTGAGCCAC
10 AGGAGCCGTGGTGCAGGACCTGCAGGCTGCTGTGGCCGCTGTCCAGAGTGCCGTCCACGAGCTGTTGGA
GTTTGCCCGCAGCGCGGTGGGCAATGCTGCCACACATGTGACCGTGCCCTGCATGCCAAGCTTAGCCGG
CAGCTGCAGAAGATGGAGGACGTGCACCCAGCCTGGTGACATGGTCAGGCCCTCGACGCTGGCCGGG
GAGGCTCTGGAGCCACCTTGGAGCCTGGACCGGCTGGTGGCTGCTCGCGGGCTGTGCCCGAGGACGC
CAAGCAGCTGGCCTCCTTCTGCACGGCAATGCCCTACTGCTCTTCAGACGGACCAAGGCCACTGCCCGG
15 GGGCCTGAGGGGGGTGGCACCCTGCACCCCAACCCCACTGACAAGACCAGCAGCATCCAGTCACGACCCC
TGCCCTCACCCCTAAGTTACCTCCCAGGACTCACCAGATGGGCAGTACGAGAACAGCGAGGGGGGCTG
GATGGAGGACTATGACTACGTCCACCTACAGGGGAAGGAGGAGTTTGAGAAGACCCAGAAGGAGCTGCTG
GAAAAGGGCAGCATCACGCGCAGGGCAAGAGCCAGCTGGAGTTGCAGCAGCTGAAGCAGTTTGAACGAC
TGAACAGGAGGTTGTCAGGCCCCATAGACCACGACCTGGCCAACTGGACGCCAGCCCAACCCCTGGCCCC
20 GGGGCGAACAGGCGGGCCTGGGGCCCTCGGACCGGCAGCTGCTGCTCTTCTACCTGGAGCAGTGTGAGGCC
AACCTGACCACACTGACCAACGCCGCTGGACGCCCTTCTTTACCGCCGTGGCCACCAACAGCCGCCCAAGA
TCTTTGTGGCGCACAGCAAGTTCGTCTATCCTCAGCGCCACAAAGCTGGTGTTCATCGGGGACACACTGTC
ACGGCAGGCCAAGGCTGCTGACGTGCGCAGCCAGGTGACCCACTACAGCAACCTGCTGTGCGACCTCCTG
CGCGCATCGTGGCCACCACCAAGGCCGCTGCCCTTGACGTACCCATCGCCTTCCGCGGCCAGGACATGG
25 TGGAGAGGGTCAAGGAGCTGGGCCACAGCACCAGCAGTTCCGCCGCGTCTTAGGCCAGCTGGCAGCCGC
CTGAGGGTGGTGACCCAGGAGGGAGGCAGGGGAGGGGTGCGGCGGTCCAGCTCCCTGGCTCCCATGTC
AAGAGTCGCTGTGCCACAGGCTTAGGGACAGGACCCAGCTCTGCGTCGGTCTCTGGTGCCTGGATGCCC
AGGAATCTGTATATTTATGGCCGGGCAGGGTGTGGGGCCATGCCCTCTCAGGAGCCGAAGCCAGGGG
CCGACGTGGCCTTCCCCAGCATGCCACCGGCCCGGTTGGGTACACAGACGGGGCTGGAGTGTGAGGG
30 TCCTGCAGCCTGCAGGACCTCGTGCCACCCCGAGGGCTGAGCCTGGTCCCACGAGGGTGCCGTGCCCT
GACAGGGCCAGTGCAGTTTGGTGTGTCTCCGCCCTTACCAGGAGAAGAACCTGAAGAACTATTTTTTCGTT
ATTGGTTTTCCAATCATTTGACTAAGAGTCTCCATTTAAATAAAGTTTTTAAAGGAA

SEQ ID NO:352

>gi|7656924|ref|NP_055382.1| breast cancer anti-estrogen resistance 1; Crk-
35 associated substrate p130Cas [Homo sapiens]
MNHLNVLAKALYDNVAESPDLSFRKGDIMTVLEQDTQGLDWWLCSLHGRQGIIVPGNRLKILVGMYYDKK
PAGPGSGPPATPAQPQPLHAPAPPASQYTPMLPNTYQPPQDSVYLVPTPSKAQQGLYQVPGPSPQFQSP
PAKQSTSTFSKQTPHHFPSPATDLYQVPPGPGGPAQDIYQVPPSAGMGHDIYQVPPSMDTRSWEGTKPPA
40 KVVVPTRVGQGYVYEAQPEQDEYDIPRHLAPGPQDIYDVPPVRGLLPSQYQGEVYDTPPMVKGPNR
DPLLEVYDVPPSVEKGLPPSNHHAVYDVPPSVSKDVPDGPPLREETYDVPPAFAKAKPFDPARTPLVLAA
PPPDSPPAEDVDVPPPPADLYDVPPGLRRPGPTLYDVPRERVLPPPEVADGGVVD SGVYAVPPPAEREA
PAEGKRLSASSTGSTRSSQSASSLEVAGPGREPLEVEAVEALARLQQGVSATVAHLDDL LAGSAGATGSW
RSPSEPQEPLVQDLQA AVAVQSAVHELLEFARS AVGNAHTSDRALHAKLSRQLQKMEDVHQTLVAHQ
45 ALDAGRGGSGATLEDLDRLVACSRAPVEDAKQLASFLHGNASLLFRRTKATAPGPEGGGTLHPNPTDKTS
SIQSRPLPSPPKFTSQDSPDGQYENSEGGWMEDYDVHLQKEFEKTQKELLEKGSITRQGSQLELQQ
LKQFERLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLLFYLEQCEANLTTLTNAVDAFFTAVA
TNQPPKIFVAHSKFVILSAHKL VFIGDTLSRQAKADVRSQVTHYSNLLCDLLRGIVATTKAAALQYPSF
SAAQDMVERVKELGHSTQQFRRVLGQLAA

SEQ ID NO:353

Perlecan
50 >GL2_37_B06_G3F1 Direction: N/A
ACCGTCTCTCTCCGAGGGCACACAACCAACCAACTGGTGTCTCTGAACAGCGCCAGTGTCCAGTTCTCTGAGG
AGCACTGGGTCCATGAGGTCTTGGNCGGGCGGTGCAGCTGCGCTGGAGCTGCTGGAGTGTGCGTGGGAAGANACTG
55 TNGAGTGGCGTGNTCATTCAAGAACNGGTGTTCCGGANGAAAACAGAACAAAGGTGGGTAGATANGGAATAAA
AGGGGGCCGATCGAATAAATCTTGAAGGCTTGAANTNAATCGTNCCAAACTTTGGAACACTTGGTCCCGGG
TTTTCAACAGTGGTGGGCGAACATTTTCTAGTCTAGTGGGACCCGGCGGTAAATAATTTCTATAAATACT
GGGCCNGTAATAAATAGATTGGAAGNGTTCACGAGTAATTTTAAACACAACATTTCCAACCATTTGTGGNGCCG
AGCGACCGAGAGTAATANTTAAGAAAAACGGGTACCGTTGGAAACCCCGTTTGGTGGGTGGAANAGTAAAAACA
60 AGACCCATTTATGAGGACGCGGGTNTATNTAACCAGCCCCAAGAANACAGGTTTAAAAAGTTTTCATGGCGACC
CAGCTTTNTTGGTCTGAAGTTNTGAAGACAAAGAATTTTTTNGGACCGNGCATTAATTTATTAATTGAGGACGGA

AAAAGAGGATTTGTGTNCGGACACAGGCGTTAAAAAATTAAATTACCGCGNATAAAAGATGAAAATAGTTGGTGC
GCCGAGGNCGAAAACGCTCGGAAAGTATTCTCNGGCAGCGCCNGTTTTTTATACCCGCAAAAAACGAAAGAGTAG
ATAATTGTGCTAGCCGGTCGTCAANTAGATGACGAATAAAATATNATAANTATGGGGTTTAAACACGTGTGGGTG
AGTAAGAGAGGAATTTAAAAAACAGGGTGTGGTTTATACATAAACATTATATTTTTATAATAGCGAATGANAGG
5 TAAAGAGACCCGGCNGGAGATAATATCTAGTGGGTACCAGATTGGTGAATAATAGGTACTGGGGTAAATTTGTT

SEQ ID NO:354

>GL2_37_B01_G3F1 Direction: N/A

ACCGCTCCTCTCCCGAGGGCACACACCCACCCAACTGGTGCTCTGAACCAGCGCCAGGTCCAGTTCTCTGAGGA
10 GCACGTGGTCCATGAGTCTGGNCGGCCGGTGCAGCGCGCGGAGCTGCTGCAGGTGCTGCAGAGCCTGGAGTGCGG
TGCTCATCCAGAACTGTGTTCTGCGAGAAACAGCACAGTGGTTAGATATGATAAAGCGGGCGCTCTGACTAAAT
CTGAGGTCTTGATACTCACTGACTGTGCTAAGGGNGGAATTCTGCGGCCGCTAAATTCAAATCTGCCCTATAN
GTGAGTCCGTATTACAATTCACCTTGGGGCGTCGTTTTACAACAGTCTGTGACTGGGAAAAAACCTGGCGTTACCC
15 ACACATTAATCTGCCCTTGCAGCGACATTCCCCTTTCTGCCAGACTGGNCGTAATAGCGAAGAGGGGCCGCGACAC
GATCTGCCCTTCCCAACAGTTGCGCAGAGCTATACGGTACAGGGGGANGATGTTAAAGCGGNTGTTACAAACGTA
TNTAAAGAGGTAAAGAAAAGAACCGCAGGGTGTGTAAATNCACGGAGGCNCTTANGGTGTATTGGTGCGCGGC
GATTTGTTTNCCTAACGGCAAGNTTGGGAATACAATTTAAATTATTGAAACAAAGNGTGACCNCGATGTGTGGTG
TGGAANAGGGAATATAGGGGTGT

SEQ ID NO:355

>GL2_37_B02_G3F1 Direction: sense

ACCGCTCCTCTCCCGAGGGCACACACCCACCCAACTGGTGCTCTGAACCAGCGCCAGGTCCAGTTCTCTGAGG
AGCACTGGGTCCATGAGTCTGGCCGGCCGGTGCAGCGCGCGGAGCTGCTGCAGGTGCTGCAGAGCCTGGAGGCCG
25 TGCTCATCCAGACCGTGT

SEQ ID NO:356

>GL2-86-1M13F Direction: sense

CTGGTGGGGATGGGGACCGCTGCCAGGGGTGAGCTGCCTTTTGCTCCACAGCCGACACTAAAGACAATTCCCA
ATCCTGAGTGGGTGGCAGAGACTCCTGCGATGCCCCGTCTCAGGTAGCTGTGGGGCACCAGCCCACAAGCCGAGGT
30 TGGCTCTCCTAGGAGTGAGAACTGCCAAGGGCTGCAGAAACAGGCCACCCAGCTCTATCTGGGGGCTCCATCGG
TGGGTAGGGGGACAGTGGGGGCAGTTCTGGGGCCACCCAGCCACTGTTCTGACCCCAAGTCTCGGTGACTTTCT
GAGGTGCCCACTCCCATCCAACCTGCCTTGCTGGCCAGCCTTGTGGCTTTGCCAGCTGTGTGTGTGAGGGTGGC
ATGCCACCTCCAGTCCAGCCAGGGCGGTA

SEQ ID NO:357

>GL2-86-2M13F Direction: sense

CTGGTGGGGATGGGGACCGCTGCCAGGGGTGAGCTGCCTTTTGCTCCACAGCGGCACTAAAGACAATTCCCA
TCCTGAGTGGGTGGCAGAGACTCCTGCGATGCCCCGTCTCANGTAGCTGTGGGGCACCAGCCCACAAGCCGAGGT
GGNTCTCCTAGGAGTGAGAACTGCCAAGGGCTGCAGAAACAGGCCACCCAGCTCTATCTGGGGGCTCCAATCGG
40 TGGGTAGGGGGACAGTGGGGGCAGTTCTGGGGCCACCCAGCACTGTTCTGAAACCAAGTCTCGGTGACTTTCTG
AGGTGCCCACTCCCATCAAACCTGGCTTGCTGGNACAGCCTTGTGGCTTTGNCCAGCTGTGTGTGTGAGGGTGGCA
TGCCCANCTCCAGTCCAGCCAGGGCGGTAGCAGCAAAGCGTGGCATCGACTCGGNNTTCTTACAAAAAATTCA
TAAATAATATTCACTAATAATATACTCGGAACATTGTGCGGGCTTGGGGGCGTTGGCCCCGGGGAGTCCAGTG
TTGGGGGGCAAGGCCAGGTTGGCCCTANACGAAGGGGGGCCAGGGGCCGTTGTGTTTGGGGCCCCGGGCCCTGGGG
45 CGCNGGTGCTTGCACAGGGC

SEQ ID NO:358

>GL2-86-3M13F Direction: sense

CTGGTGGGGATGGGGACCGCTGCCAGGGGTGAGCTGCCTTTTGCTCCACAGCGGCACTAAAGACAATTCCCA
ATCCTGAGTGGGTGGCAGAGACTCCTGCGATGCCCCGTCTCAGGTAGCTGTGGGGCACCAGCCCACAAGCCGAGGT
50 TGGCTCTCCTAGGAGTGAGAACTGCCAAGGGCTGCAGAAACAGGCCACCCAGCTCTATCTGGGGGCTCCATCGG
TGGGTAGGGGGACAGTGGGGGCAGTTCTGGGGCCACCCAGCACTGTTCTGAAACCAAGTCTCGGTGACTTTCT
GAGGTGCCCACTCCCATCAAACCTGCCTTGCTGGCCAGCCTTGTGGCTTTGCCAGCTGTGTGTGTGAGGGTGGC
ATGCCACCTCCAGTCCAGCCAGGGCGGTAGCAGCAAAGCGTGGCATCGCCTCGGTTTCTTACAAAAAATTCA
55 ATAATATTAATAATAATATACTCGACATTGTGCGGCTGG

SEQ ID NO:359

>GL2-86-5M13F Direction: sense

CTGGTGGGGATGGGGACCGCTGCCAGGGGTGAGCTGCCTTTTGCTCCACAGCGGCACTAAAGACAATTCCCA
ATCCTGAGTGGGTGGCAGAGACTCCTGCGATGCCCCGTCTCAGGTAGCTGTGGGGCACCAGCCCACAAGCCGAGGT
60

TGGCTCTCCTAGGAGTGAGAACTGCCCAAGGGCTGCAGAAACAGGCCACCCAGCTCTATCTGGGGGCTCCATCGG
TGGGTAGGGGACAGTGGGGGAGTTCTGGGCCACCCAGCCACTGTNCCTGACCCCAAGTCCTGGTGACTTTCT
GAGGTGCCCACTCCACATCCAACCTGCCTTGCTGGNCAGCCTTGNTGGCATAATGCCAGNCTGATAGATGCGTG
AGGGNGGACATGCCACCTACCAGTACCAGACCCAGGGCGGATAGGCAGCAAAGNACGTGGCATCGCCTCGGG

SEQ ID NO:360

>GL2-86-1M13R Direction: N/A

CTGGTCAGCGGCCGGTCCCCAGGTCCCAACGTGGCAGTCAACGCCAAGGGCAGCGTCTACATCGGCGGAGCCCCCT
GACGTGGCCACGCTGACCGGGGAGATTCTCTCGGGCATCACAGGCTGTGTCAAGAACCTGGTGCTGCACTCG
GCCCCGACCCGGCGCCCCGCCCCACAGCCCCCTGGACCTGCAGACCGGGCCAGGCCGGGGCCAAACACAGCCCCCTG
CCCCCTCGTAGGCACCTGCCTGCCCCACAGGACTCCCGGGCCACGCCCCAGCCCGACAATGTCGAGTATATTATT
ATTAATATTATTATGAA

SEQ ID NO:361

>GL2-86-2M13R Direction: N/A

CTGGTCAGCGGCCGGTCCCCAGGTCCCAACGTGGCAGTCAACGCCAAGGGCAGCGTCTACATCGGCGGAGCCCCCT
GACGTGGCCACGCTGACCGGGGAGATTCTCTCGGGCATCACAGGCTGTGTCAAGAACCTGGTGCTGCACTCG
GCCCCGACCCGGCGCCCCGCCCCACAA

SEQ ID NO:362

>GL2-86-3M13R Direction: N/A

TTGGTCAGCGGCCGGTCCCCAGGTCCCAACGTGGCAGTCAACGCCAAGGGCAGCGTCTACATCGGCGGAGCCCCCT
GACGTGGCCACGCTGACCGGGGAGATTCTCTCGGGCATCACAGGCTGTGTCAAGAACCTGGTGCTGCACTCG
GCCCCGACCCGGCGCCCCGCCCCACAGCCCCCTGGACCTGCAGACCGCGCCAGGCCGGGGCCAAACACAGCCCCCT
TGCCCCCTCGTAGGCACCTGCCTGCCCCACAGGACTCCCGGGCCACGCCCCAGCCCGACAATGTCGAGTATATTAT
TTATTAATATTATTATGAATTTTNNGTAAAGAAACCGAGGCGATGCCACGCTTANGCTGCTACCGCCCTGGGCTGG
ACTGGAGGTGGGCATGCCACC

SEQ ID NO:363

>GL2-88-5M13R Direction: anti-sense

CTGGTCAGCGGCCGGTCCCCAGGTCCCAACGTGGCAGTCAACGCCAAGGGCAGCGTCTACATCGGCGGAGCCCCCT
GACGTGGCCACGCTGACCGGGGAGATTCTCTCGGGCATCACAGGCTGTGTCAAGAACCTGGTGCTGCACTCG
GCCCCGACCCGGCGCCCCGCCCCACAGCCCCCTGGACCTGCAGACCGCGCCAGGCCGGGGCCAAACACAGCCCCCT
GCCCCCTCGTAGGCACCTGCCTGCCCCACAGGACTCCCGGGCCACGCCCCAGCCCGACAATGTCGAGTATATTATT
ATTAACATATTATTATGAATTTTGTAAAGAAACCGAGGCGATGCCACGCTTTGCTGCTACCGCTGGGGCTGGGA
CTGGAGGTGGGCATGCCAACACCATCACGGCACAACAGCTGGCAAAAGCCAACAAAGGGCCTTGGGCCAGGCAAG
GGCACAGGTGGGACTGGGAGTGGGGCACCCCTCANGAAAGGTACCCAGGGAACATATGGGGGGGTNCCAGAGGAA
ACCACAGGTAGGGGACCTGGGGGTTTNGGGGGCCCCCAGGAAAACCTTGGGGCGCCCAAAANATNGNTACCACC
ACCATAAACACACAAGCCAGAANTGTGAAAACCCCCAACCCAGAGAAANTAGCAGAGCCATCGAGGAAAGCACC
CCAAGATACACAGCANNACCCCATGAGAA

SEQ ID NO:364

>GL2_93_2B09_G3F1 Direction: N/A

AAGCTGCCTTTTGCTCCACAGCCGGCACTAAAGACAATTCCAATCTGAGTGGGTGGCAGAGACTCCCTTTGGG
GCGATGCCCGTCTTCCAGGTAAGGCTGTGGTGGGCGGGCCAACACACCAAAAAGGGGCCCCCCCCAAATAGCC
CCATACAAAACAAAACACNGGGGGCCATACCCACGGGAAAAGGGGGTTTATGGGTGGGCCATTTTCCCCCAGT
TTCCACCCGTTTAAACAGGCGNGGCAACACNGCTTTTGGGCGTGNCTGGAACAACAACCCCTTTTGGGTCTCCTCC
NCCCAAAAAGTAGGGTGGGCTGGGCGGCCCTTTTATGTGTGGCCCAANACNGGAGAACACAATACTAAATAATC
CCAACTGGTGTGGGGTGTCCCGCCCAATANACCCACCCCAANTAGATGCCCTTTTACCCCGTTTATAAAA
AATTTTTTTTTTCCCCCTATATCTTGGCGGGGGCGAGGGGATATGT

SEQ ID NO:365

>gi|7427516|ref|NM_005529.2| Homo sapiens heparan sulfate proteoglycan 2
(perlecan) (HSPG2), mRNA

GCCCCGAGCGAGCGAGAGAGCGGCGCGGGCCGGCCATGGGGTGGCGGGCGCCGGGCGCGTCTGCTG
CTGGCGCTGCTGCTGCACGGGCGGCTGCTGGCGGTGACCATGGGCTGAGGGCATAACGATGGCTTGTCTC
TGCCCTGAGGACATAGAGACCGTCACAGCAAGCCAAATGCGCTGGACACATTCTGATACCTTTCTGATGATGA
GGACATGCTGGCTGACAGCATCTCAGGAGACGACCTGGGCGAGTGGGGACCTGGGCAGCGGGGACTTCCAG
ATGGTTTATTTCGAGCCCTGGTGAATTTCACTCGCTCCATCGAGTACAGCCCTCAGCTGGAGGATGCAG
GCTCCAGAGAGTTTCGAGAGGTGTCCGAGGCTGTGGTAGACACGCTGGAGTCCGAGTACTTGAAAATTC

CGGAGACCAGGTTGTCAGTGTGGTGTTCATCAAGGAGCTGGATGGCTGGGTTTTTGTGGAGCTGGATGTG
GGCTCGGAAGGGAATGCGGATGGGGCTCAGATTACAGGAGATGCTGCTCAGGGTCATCTCCAGCGGCTCTG
TGGCCTCCTACGTACCTCTCCCCAGGGATTCCAGTTCCGACGCCTGGGCACAGTGCCCCAGTTCCCAAG
AGCCTGCACGGAGGCCGAGTTTGCCTGCCACAGCTACAATGAGTGTGTGGCCCTGGAGTATCGCTGTGAC
5 CGGCGGGCCCGACTGCAGGGACATGTCTGATGAGCTCAATTGTGAGGAGCCAGTCTTGGGTATCAGCCCCA
CATTCTCTCTCTCTCGTGGAGACGACATCTTTACCGCCCCGGCCAGAGACAACCATCATGCGACAGCCACC
AGTCACCCACGCTCCTCAGCCCCCTGCTTCCCGGTTCCTGTCAGGCCCCCTGCCCTGTGGGCCCCAGGAGGCC
GCATGCCGCAATGGGCACTGCATCCCCAGAGACTACCTCTGCGACGGACAGGAGGACTGCGAGGACGGCA
CGATGAGCTAGACTGTGGCCCCCGCCACCCTGTGAGCCCAACGAGTTCCCCCTGCGGGAATGGACATTG
10 TGCCCTCAAGCTGTGGCGCTGCGATGGTGACTTTGACTGTGAGGACCGAACCTGATGAAGCCAAGTGGCCCC
ACCAAGCGTCTGAGGAAGTGTGCGGGCCACACAGTTCCGATGCGTCTCTACCAACATGTGCATCCAG
CCAGCTTCCACTGTGACGAGGAGAGCGACTGTCTGACCGGAGCGACGAGTTTGGCTGCATGCCCCCCA
GGTGGTGACACCTCCCCGGGAGTCCATCCAGGCTTCCCGGGGCCAGACAGTGACCTTCACCTGCGTGGCC
ATTGGCGTCCCCGCCCCCTTTCTCATCAATTGGAGGCTCAACTGGGGCCACATCCCTCTCAGCCAGGG
15 TGACAGTGACCAGCGAGGGTGGCCGTGGCACACTGATCATCCGTGATGTGAAGGAGTCAGACCAGGGTGC
CTACACCTGTGAGGCCATGAACGCCCCGGGGCATGGTGTGTTGGCATTCCTGACGGTGTCTTTGAGCTCGTC
CCACAACGAGCAGGCCCCCTGCCCTGACGGCCACTTCTACCTGGAGCACAGCGCCGCTGCTGCCCCGTCT
TCTGCTTTGGCATCACCAGCGTGTGCCAGAGCACC CGCGCTTCCGGGACCAGATCAGGCTGCGCTTTTGA
CCAACCCGATGACTTCAAGGGTGTGAATGTGACAATGCCCTGCGCAGCCCGGCACGCCACCCCTCTCTCTCC
20 ACGCAGCTGCAGATCGACCCATCCCTGCACGAGTTCCAGCTAGTCGACCTGTCCCGCCGCTTCTCTGCTCC
ACGACTCCTTCTGGGCTCTGCTTGAACAGTTCTTGGGCAACAAGGTGGACTCCTATGGCGGCTCCCTGCG
TTACAACGTGCGCTACGAGTTGGCCCCGTGGCATGCTGGAGCCAGTGACGCGCCGGACGTGGTCTCTGTC
GGTGCCGGGTACCGCTCCTCTCCCGAGGCCACACACCCACCCAACCTGGTGTCTGTAACCAGCGCCAGG
TCCAGTTCTCTGAGGAGCACTGGGTCCATGAGTCTGGCCGGCCGCTGCAGCGCGCGGAGCTGCTGCAGGT
25 GCTGCAGAGCCTGGAGGCCGTGCTCATCCAGACCGTGTACAACACCAAGATGGCTAGCGTGGGACTTAGC
GACATCGCCATGGATACCACCGTCACCCATGCCACAGCCATGGCCGTGCCACAGTGTGGAGGAGTGCA
GATGCCCCATTGGCTATTCTGGCTTGTCTGCGAGAGCTGTGATGCCACTTCACTCGGGTGCCTGGTGG
GCCCTACCTGGGCACCTGCTCTGGTTGCAATGGCCATGGCCAGCTCCTGTGACCCCTGCTGTATGGC
CACTGCCTGAATTGCCAGCACAAACGAGGGGCCACAGTGCAAGAAGTGCAAGGCTGGCTTCTTTGGGG
30 ACGCCATGAAGGCCACGGCCACTTCTGCGCGCCCTGCCCTTGCCCATACATCGATGCCTCCCGCAGATT
CTCAGACACTTGTCTCTGACACGGATGGCCAAGCCACATGTGACGCTGTGCCCCAGGCTACACTGGC
CGCCGCTGTGAGAGCTGTGCCCCCGGATACGAGGGCAACCCATCCAGCCCGCGCGGAAGTGACAGCCCCG
TCAACCAGGAGATTGTGCGCTGTGACGAGCGTGGCAGCATGGGGACCTCCGGGGAGGCCCTGCCGCTGTAA
GAACAATGTGGTGGGGCGCTTGTGCAATGAATGTGCTGACCGCTCTTTCCACCTGAGTACCCGAAACCCC
35 GATGGCTGCCCTCAAGTGCTTCTGCATGGGTGTGCTGCGCACTGCACAGCTCTTCATGGAGCCGTGCC
AGTTGCATGGGGCCCTCTGAGGAGCCTGGTCACTTGCAGCTGACCAACGCGCAAGCACCCACACCACCAA
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SEQ ID NO:366

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PGR-1 (T-cell activation protein)

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>GL3_26KV_PCR_G3F1 Direction: N/A

30 ATATGCTCATCCAGATCAAAACGCAGGTGGAGGCCTCGGAGGAGAGCGCCCTCAACCACCTCCAGAACC CGGGCG
 ACGCGGCCGAGGGCCGGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCAAGGGAGATTGCGAAGATGGCA
 GAGATGCTGGTGGAGCTGGTCCGGCGGATAGAGAAGAGCGAGTCGTCTGAGCGCGGTTCGGCGGTTTTCCAGCCAA
 35 TGGATTCTGGTCAACTGGTGGAGATTGGCTGACACCCTGGAGAAGCCGAAACCAGAGAGCCTTTTGTCTTCTCTT
 TTTTTCTCTGTCTATGCTCTGTCTCACTTTAACTACTACGTTTTCTGCTATGGGTCTCTGGTGAGATTGATGACC

SEQ ID NO:369

>GL3_27BP_3_M13F Direction: N/A

40 ATATGCTCATCCAGATCAAAACGCAGGTGGAGGCCTCGGAGGAGAGCGCCCTCAACCACCTCCAGAACC CGGGCG
 ACGCGGCCGAGGGCCGGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCAAGGGAGATTGCGAAGATGGCA
 GAGATGCTGGTGGAGCTGGTCCGGCGGATAGAGAAGAGCGAGTCGTCTGAGCGCGGTTCGGCGGTTTTCCAGCCAA
 TGGATTCTGGTCAACTGGTGGAGATTGGCTGACACCCTGGAGAAGCCGAAACCAGAGAGCCTTTGTGTTTCTCTC
 TTTTTTTTCCCTGTCTATGCTCTGTCTCACTTAACACTACGTTTTCTGCTATGGTCATGTGGTTGATGACCTC
 45 AATATGAGTTTTCGAATGGTAACGTGTATAGAGTAGTGGGAAGTAATTTGGTTTGAANAATGCTCTCACAATACAG
 GGAATTAGGGACCTAGGATTGTAAGCTCTTGCCAGGCAGGTCAACATTTTGTTCCTGGGGCTTTGGGGGGTAATT
 TCTA

SEQ ID NO:370

>GL3_27BP_3_M13R Direction: anti-sense

50 CCCCCTTGAAGTCTGGTCCCTTTCTTCAGTAGTTGCTGCTAGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCAG
 CACCTCCAGAGCTGGAGAACTCCAAGTGTGAGTCTCATGTGTACACACAGACCCAAAGTTCCAGGGAGCTATCA
 GGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCAACAAAGCCCGGGAACAAATGTGAGTCT
 GCAAGAGCTTACAATCTAGGTCTTAATTCCTGTATGTGAGAGCATTTTCAAACAAAATTACTTCCCAAACAAAA
 CACGTTAACAATCGAAACTCATATTGAGGTCAACACAGACCATAGCAGAAAACGTAGTGTTAAGTGAGACA
 55 GAGCATAGACAGGAAAAAAGAGAAAAACAAAGGCTCTCTGGTTTTCGGCTTCTCCAGGGTGTGAGCCAATCTCC
 ACCAGTTGACCAGAATCCATTGGCTGGAAACCGCCGACCGCGCTCACGACGACTCGCTCTTCTCTATCCGCCGGA
 CCAGCTCCACCAGCATCTTCTGCCATCTTCGCAATCTCTTGGCCTTCTCTCGGCTTCTCGCACCTCTT

SEQ ID NO:371

>GL3_8D_1_M13R Direction: anti-sense

CCCCGTTGAAGTCTGATCCTTTCTTCAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCAG
CACCTCCAGAGCTGGAGAAGTCCAAGTGTGAGTCTCATGTGTACACACAGACCCAAAGTTCCAGGGAGCTATCA
GGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTGCT
GCAAGAGCTTACAATCTAGGCCCTAATTCCTGTATGTGAGAGCATTTCAAACAAAATTACTTCCCAAACAAAA
CACGTTAACAATCGAAACTCATATTGAGGTCAACACAGACCATAGCAGAAAACGTAGTGTAAAGTGAGACA
GAGCATAGACAGGAAAAAAGAGAAAAACAAAGGCTCTCTGGTTTCGGCTTCTCCAGGGTGTGAGCCAATCTCC
ACCAGTTGACCAGAATCCATTGGCTGGAAC

SEQ ID NO:372

>GL3_8D_2_M13R Direction: anti-sense

CCCCGTTGAAGTCTGGTCCTTTCTTCAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCAG
CACCTCCAGAGCTGGAGAAGTCCAAGTGTGAGTCTCATGTGTACACACAGACCCAAAGTTCCAGGGAGCTATCA
GGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTGCT
GCAAGAGCTTACAATCTAGGCCCTAATTCCTGTATGTGAGAGCATTTCAAACAAAATTACTTCCCAAACAAAA
CACGTTAACAATCGAAACTCATATTGAGGTCAACACAGACCATAGCAGAAAACGTAGTGTAAAGTGAGACA
GAGCATAGACAGGAAAAAAGAGAAAAACAAAGGCTCTCTGGTTTCGGCTTCTCCAGGGTGTGAGCCAATCTCC
ACCAGTTGACCAGAATCCATTG

SEQ ID NO:373

>GL3_8D_3_M13R Direction: anti-sense

CCCCGTTGAAGTCTGGTCCTTTCTTACAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCA
GCACCTCCAGAGCTGGAGAAGTCCAAGTGTGAGTCTCATGTGTACACACAGACCCAAAGTTCCAGGGAGCTATC
AGGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTGC
TGCAAGAGCTTACAATCTAGGCCCTAATTCCTGTATGTGAGAGCATTTCAAACAAAATTACTTCCCAAACAAAA
ACACGTTAACAATCGAAACTCATATTGAGGTCAACACAGACCATAGCAGAAAACGTAGTGTAAAGTGAGAC
AGAGCATAGACNGGAAAAAAGAGAAAAACAAAGGCTCTCTGGTTTCGGCTTCTCCAGGGTGTGAGCCAATCTC
CACCAGTTGGCCAGAATCCATTGGCTGGAACCGCCGACCGCTCAGACGACTCGCTCTTCTATCCGCCG
ACCAGCTCCACCAGCATCTCTGCCATCTTC

SEQ ID NO:374

>GL3_8D_4_M13F Direction: N/A

AATATGCTCATCCAGATCAAAACGCAGGTGGAGGCCTCGGAGGAGAGCGCCCTCAACCACCTCCAGAACCCGGGC
GACGCGGCCGAGGGCCGGGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCAAGGAGATTGCGAAGATGGCA
GAGATGCTGGTGGAGCTGGTCTGGCGGATAGAGAAGAGCGAGTCGTCTGAGCGCGGTTCGGCGGTTTCCAGCCAA
TGGATTCTGGTCAACTGGTGGAGATTGGCTGACACCCTGGAGAAGCCGAAACAGAGAGCCTTTTGTCTTCTCTT
TTTTTCTCTGCTATGCTCTGTCTCACTTAACACTACGTTTTCTGCTATGGTCTGTGGTTGATGACCTCAATATG
AGTTTCGATGTGTTAACGT

SEQ ID NO:375

>GL3_8D_4_M13R Direction: anti-sense

CCCCGTTGAAGTCTGGTCCTTTCTTCAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCA
GGCACCTCCAGAGCTGGAGAAGTCCAAGTGTGAGTCTCATGTGTACACACAGACCCAAAGTTCCAGGGAGCTAT
CAGGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTG
CTGCAAGAGCT

SEQ ID NO:376

>GL3_8D_PCR_G3F1 Direction: N/A

ATATGCTCATCCAGATCAAAACGCAGGTGAGGCCTCGGAGGAGAGCGCCCTCAACACCTCCAGAACCCGGGCGA
CGCGCGGAGGCCGGGCGGGCAAAAGTGCAGAGAAGGCCGAGGAGAAGGCCAGGAGATTGCGAAGATTGCAGAGAT
GCTGGTGGAGCTGGTCCGGCGATAGAGAAGAGCGAGTCGTCTGAGCGCGGTTCGGCGGTTTCCAGCCCATGGAT
TCTGGTCAACTGGTGGAGATTGGCTGACACCCTGGAGAAGCCGAAACAGAGAGCCTTTTGTCTTCTCTTTTTT
TCCTGTCTATGCTCTGTCTCACTTAACACTACGTTTTCTGCTATGGTCTGTGGTTGATGACCTCAATATGAGTTT
CGATTGTTAACGTGTTTTTGTGGGAAGTAATTTTGTGAAAATGCTCTCACATACAGGAATTA

SEQ ID NO:377

>gi|15193293|ref|NM_033296.1| Homo sapiens T-cell activation protein (PGR1), mRNA

TTGTCCGTGGCTTCTCTGAGAAGAAAAGTTGAAAAAGGGTAAAAGTTTTTCAGGAATATTCGGGCTCTCTA

TTGCTAAGCATAGCGAGTGTGCGGTTTTCTCTCTCCAACAGACATCGCTATTGCGGTTCCGAGGCAGTGGG
AAGAGATGCGGCCCCCTGGACATCGTCGAGCTGGCGGAACCGGAGGAAGTGGAGGTGCTGGAGCCCCGAGGA
GGATTTTCGAGCAGTTTCTGCTCCCGGTCAACGAGATGCGCGAGGACATCGCGTCGCTGACGCGCGAG
5 CACGGGCGGGCGTACCTGCGGAACCGGAGCAAGCTGTGGGAGATGGACAATATGCTCATCCAGATCAAAA
CGCAGGTGGAGGCCTCGGAGGAGAGCGCCCTCAACCACCTCCAGAACCCGGGCGACGCGGCCGAGGGCCG
GGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCAAGGAGATTGCGAAGATGGCAGAGATGCTGGTG
GAGCTGGTCCGGCGGATAGAGAAGAGCGAGTCGTCGTGAGCGCGGTCGGCGGTTTCCAGCCAATGGATTTC
TGGTCAACTGGTGGAGATTGGCTGACACCCCTGGAGAAGCCGAAACCAGAGAGCCTTTGTGTTTTCTTTTT
10 TTCTGTCTATGCTCTGTCTCACTTAACACTACGTTTCTGCTATGGTCTGTGGTTGATGACCTCAATAT
GAGTTTCGATTGTTAACGTGTTTTTGTGTTGGGAAGTAATTTGTTTGAAAATGCTCTCACATACAGGAAT
TAGGGCCTAGATTGTAAGCTCTTGCAGCAGTCACATTTGTTCCCGGGCTTTGGTGGTTATTTCTAAATTT
TTGAGGTGCTTTGCTATTTCTTGTGTGACCTGATAGCTCCCTGGAACTTTGGGTCTGTGTGTGACACATG
AGACTCACAGTTGGAGTTCTCCAGCTCTGGAGGTGCTGAAGGAGCTGCATTAATTCTGGAAGACGACTCC
15 ATGCAGCAACTACTGAAGAAAGGACCAGACTTCAACGGGGAGTGTGGATGGGCCGACCTGGCTGGGACTC
TGGAATCTGGAGAAGAGCTGGAGAATGGATAGTATTGTCTGTATTGAGAGACTTTAATTTCTGTGTGAGA
CCAAAGGAGGAGAGATGTGTTTTGTTCAAATTTAAATTTGTTGTGGTACACTATCTTATGTAACCTGTC
TGGTGAGTTTGTGTTGGACAACCTAAGCTGTTTATTTGACATGGAACCTAAAATAGAAGATAAGATCTT
GATATTCTGTACAAGTTGATGTAATACCTGATGCGTTTATAGAGGACTTGGCATAAAATGAAAGATTGGC
AAAGGCCCTTGAGGGGCTTGGGGATGACAGTATGGAACCTGCTGCTGATTTGAGACCTAACTGGACTAGAAG
20 AGGCATCTTCAAGGTTTACATCGTTGTCCAGCTGTAAGTTCATTTGAGTAGCAGACCTAACAAATTTGA
GGTCAGAACCCTACCATGTTAAAACAAACAAAACCTTACCATGTTAATAAAAGTATTCATTTGC

SEQ ID NO:378

25 >gi|15193294|ref|NP_150638.1| T-cell activation protein [Homo sapiens]
MRPLDIVELAEPEEVEVLEPEEDFEQFLLPVINEMREDIASLTREHGRAYLRNRSKLWEMDNMLIQIKTQ
VEASEESALNHLQNPGDAAEGRAAKRCEKAEEKAKEIAKMAEMLVELVRRRIEKSESS

SEQ ID NO:379

Phosphoribosyl pyrophosphate synthetase-associated protein 1
30 >GL3_38B_PCR_G3F1 Direction: N/A
CGCCCGCCCCGTTCCCCCGCCGGCCATGAACGCCGCTCGCACCGGCTACCGAGTCTTCTCGGCCAACTCCACGGC
CGCCTGCACGGAGCTGGCCAAGCGCATCACAGAGCGCCTTGGTGCTGAATTGGGGAAGTCTGTTGTATATGAAGA
GACCAATGGAGAAACAAGAGTTAAAATAAAAGAATCTGTTGCTGGCCAAGATATTTTCATTATACAGACAATACC
35 CAGAGATGTGAATACAGCTGTGATGGAGTTGCTCATCATGGCTTACGCACTGAAGACTGCCTGTGCCAGGAACAT
TATTGGGGTCATCCCCTACTTCCCCTACAGCAAGCAGAGCAAGATGAGAAAGAGGGGTTCCATTGTGTGCAAGCT
GCTAGCATCCATGCTGGCGAAAGCAGGTTAACTCACATTATCACTATGGATCTTCATCAAAAGGAAATACAAGG
CTTTTTTCAGCTTTCCTGTGGACAACCTTAGAGCCTCACCTTTCCTGCTTCAGTATATCCGGAAGAAATCCAAAT
TACAGAAATGCAGTCATTGTAGCTCTCCTGATGCTGCAAGAGGGCCAGTCCTATGCGGAGAGACTGCGTC
40 TGGGTTTTGGCCGTCATTACGGGGAAGCTCAGTGCACGGAAGTGG

SEQ ID NO:380

>GL3_8K_2_M13R Direction: sense
CTGCCCCGGCCCCGTTCCCCCTGCCNGGCCATGAACGCCGCTCGCACCGGCTACCGAGTCTTCTCGGCCAACTC
45 CACGGCCGCTGCACGGAGCTGGCCAAGCGCATCACAGAGCGCCTTGGTGCTGAATTGGGGAAGTCTGTTGTATA
TGANAGAGACCAATGGAGGAAACCAAGAGTTACACANAGTACAAAGAANTCTGTTGCTTGGCCAAGGATATTTTC
ATTATACAGACAATTAACCCAGAGATGTGAATACAGCTGTGATGGAGTTGCTCATCATGGCTTACGCACTGAAGA
CTGCCCTGTGCCAGGAAC

SEQ ID NO:381

50 >GL3_8K_3_M13R Direction: sense
CGCCCGCCCCGTTCCCCCGCCGGCCATGAACGCCGCTCGCACCGGTACCGAGTCTTCTCGGCCAACTCCACGGCGCC
TGACGGAGCTGGCCAAGCGCATACAGAGCGCCTTGGTGCTGAATTGGGGAAGTCTGTTGTATATTAAGAGACCAA
TGGGAAACAAGAGTTAAATAAAAGATCTGTTGCTGG

SEQ ID NO:382

55 >GL3_8K_4_M13F Direction: anti-sense
CGCCCGCCCCNGTTTCCCCCGCCGGCCATGAACGCCGCTCGCACCGGTACCGAGTTCTTCTCGGCCAACTCCAC
GGCCGCTGCACGGAGCCTTGGCCAAGCCGCATCACAGAGCGCCTTGGTGCTGAATGGGGAAGTCTGTGGTATA
TGAAGAGACCAATGGAGGAAACAAGAGTTAAAATAAAAGAATTCTGTTGCTTGGCCAAGATATTTTCATTATATA
60 CAGACAATTACCCAGAGATGTTGAATTACAGCTTGTGATTGGAGTTTGCTCATTCATGGCTTTACGCCACTGAA

GACTTGCCTTGTGGCCAGGAACATTTATTGGGGTCATCCCCCTACTTCCCCCTACAGCAAGCAGAGCAAAGATGAG
AAAGAGGGGTTCCATTGTGTGCAAGCTGCTTAGGCAATCCATGCTGGCCGAAAAGCNGGTTTAACTCACATTATC
ACTATGGATCTTCATCAAAGGAAATACAAGGGCTTTTACAAGCTTTCCTTGTGGAACAAACCCCTTTAGAAGCCT
TCAACCTTTTTCTGCTTCAGTATATCCCAGGAAGGAAATCCAAATTACCAGAAATGCAGGTCAATTTGGTAGCT
AAGTCTCCCTGATGCCTTGCCAAGGANGGGCCAGTCCTATTTCGGAGAANACATGCGTCTGGTTGGGCCGGAANTC
ACACGGGAAACCNCATGCACAGAACTCNGGACCTTGG

SEQ ID NO:383

>GL3_8K_PCR_G3F1 Direction: N/A

CGCCCCGCCCCGGTTCCCCGCCGGCCATGAACGCCGCTCGCACCCGGCTACCGAGTCTTCTCGGCCAACTCCACGGC
CGCCTGCACGGAGCTGGCCAAGCGCATCACAGAGCGCCTTGGTGCTGAATTGGGGAAGTCTGTTGTATATGAAGA
GACCAATGGAGAAACAAGAGTTAAAATAAAAGAATCTGTTTCGTGGCCAAGATATTTTCATTATACAGACAATACC
CAGAGATGTGAATACAGCTGTGATGGAGTTGCTCATCATGGCTTACGCACTGAAGACTGCCTGTGCCAGGAACAT
TATTGGGGTCATCCCCCTACTTCCCCCTACAGCAAGCAGAGCAAGATGAGAAAGAGGGGTTCCATTGTGTGCAAGCT
GCTAGCATCCATGCTGGCGAAAGCAGGTTTAACTCACATTATCACTATGATCTTCATCAAAGGAAATACAAGGC
TTTTTCAGCTTTCTGTGGACAACCTTAGAGCCTCACCTTTCTGCTTCAGTATATCCGGAAGAAATCCAAATT
ACAGAAATGCAGTCATTGTAGCTAACGTCTCCTGATGCTGCAAAGAGGGCCAGTCCTATGCGGAGAGACTGCGT
CTGGGTTTGGCCGTCATTACGGGGAAGCTCAGTGCACGGAACCTGGACATTGGACGATGGTTCGTCAACTCCCCGC
TATGGTCAAATGCTACTGTGCACCC

SEQ ID NO:384

>gi|4506130|ref|NM_002766.1| Homo sapiens phosphoribosyl pyrophosphate
synthetase-associated protein 1 (PRPSAP1), mRNA

GGTGCAGCAAGGGCACGGACCTCGGAGCTCTCCCCGTTCCCCCGCCGGCCATGAACGCCGCTCGCACCCGGC
TACCGAGTCTTCTCGCCAACCTCCACGGCCGCTGCACGGAGCTGGCCAAGCGCATCACAGAGCGCCTTG
GTGCTGAATTGGGGAAGTCTGTTGTATATCAAGAGACCAATGGAGAAACAAGAGTTGAAATAAAAGAATT
TGTTTCGTGGCCAAGATATTTTCATTATACAGACAATACCCAGAGATGTGAATACAGCTGTGATGGAGTTG
CTCATCATGGCTTACGCACTGAAGACTGCCTGTGCCAGGAACATTATTGGGGTCATCCCCCTACTTCCCCCT
ACAGCAAGCAGAGCAAGATGAGGAAGAGGGGTTCCATTGTGTGCAAGCTGCTAGCATCCATGCTGGCGAA
AGCAGGTTTAACTCACATTATCACTATGGATCTTCATCAAAGGAAATACAAGGCTTTTTTCAGCTTTCTT
GTGGACAACCTTAGAGCCTCACCTTTCTGCTTCAGTATATCCAGGAAGAAATCCAAATTACAGAAATG
CAGTCATTGTAGCTAAGTCTCCTGATGCTGCAAAGAGGGCCAGTCCTATGCGGAGAGACTGCGTCTGGG
TTTGGCCGTCATTACGGGGAAGCTCAGTGCACGGAACCTGGACATGGACGATGGTTCGTCACCTCCCCGCT
ATGGTCAAAAATGCTACTGTGCACCCAGGCCTGGAGTTGCCATTGATGATGGCCAAAGAGAAGCCACCGA
TAACTGTAGTTGGAGATGTTGGAGGCCGCATCGCAATCATCGTGGATGACATTATTGACGATGTGGAGAG
TTTTGTGCTGCCGCGGAGATCCTGAAAGAGAGAGGGCGCCTATAAGATCTATGTTATGGCCACCCACGGC
ATCCTGTCTGCAGAGGCCCTCGCCTGATTGAGGAGTCTCCGTAGACGAGGTGGTGGTGACGAATACTG
TCCCTCATGAGGTTTCAAGAGCTGCAATGTCCCAAGATAAAGACTGTGGATATCAGTTTGATTCTTTCTGA
AGCCATTCCGAGAAATCCACAATGGAGAGTCCATGGCCTACCTTTTCCGAAACATCACTGTGGATGACTAG
CTTTCACGAGGGTCTCGACCCTGGACCTCCTGAGGGAAACATGGAAAAAGCAGTGCCATGATGATACAG
TGTTTCTTGCAGGGGAGGACTCGAAACAGCCTGGAGTTAGATATCTTCTTTTGGCCGGATTGATGGGGA
GGAGGGATTAAAGAGTCAAGGAAGAAGACAGAGCTAATGGATAAATATCATAACATGGCCTTACATGTCT
GCTGTATCAGCCCTGTTTCTTAAAGTTCTAGCTGCTTTCTTAAATAATCTGAAAATCTTATTGATA
CTAAAGAGGAGTTAAAGGCACATAAAGTCTTAACTCTATAATGTTTCAATTTAGTTGTTTCAGCTCCAGGGA
AATGGAGGTATTGATGTTGAACCTGGTTAGGGAAGCTGAGCGCCTGTGGCCCTATTACTATCCAGTTGGC
CTCTCCCAAATCAACTTCAAGTCTTTTATAGAGAATCGTATTTTCTTTCAGAAATTGCTATGCCTACAG
CCATTGAAAAATGAAGCATTATGTTGTTACATCTTCCAAGGATGTGAGATTAGAAAAATAGCATCCCACC
TCTGGGTATCTGAGTGGCTCTGAAGTTGCAATAAAATAATTTGTTGT

SEQ ID NO:385

>gi|4506131|ref|NP_002757.1| phosphoribosyl pyrophosphate synthetase-
associated protein 1 [Homo sapiens]

MNAARTGYRVFLANSTAACTELAKRITERLGAE LGKSVVYQETNGETRVEIKEFVRGQDIFIQTIPRDV
NTAVMELLIMAYALKTACARNIIGVIPYFPYSKQSKMRKRSIVCKLLASMLAKAGLTHIITMDLHQKEI
QGFFSFPVDNLRASPFLQYIQEEIPNYRNAVIVAKSPDAAKRAQSYAERLRLGLAVIHGEAQCTELDMD
DGRHSPPMVKNATVHPGLEPLMMAKEKPITVVGDVGGRIAIIVDDIIDDVESFVAAAAILKERGAYKI
YVMATHGILSAEAPRLIESSVDEVVVTNTVPHEVQKLQCPKIKTVDISLILSEAIRRIHNGESMAYLFR
NITVDD

SEQ ID NO:386

Plakoglobin

>G3_1_90_PCR_G3F1 Direction: N/A

GTGCGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCACAACCTCTCCAC
CACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTTCTCTGGTCCGCATGCTCAGCTCCCCTTT
GAGTCGGTCTGTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATGGCCGTG
CGCCTGGCCGACGGGCTGCAAAAGATGGTGCCCTGCTCAACAAGAACAACCCCAAGTTCCTGGCCATCACCACC
GACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGTGGGCCCCAGGGC
CCTCGGTGCACGATTATGCGTTACTTCGTTTTAAAGC

SEQ ID NO:387

>G3_4_01_PCR_G3F1 Direction: N/A

CCAGTGCTGTGCTGGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCAC
AACCTCTCCACCACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTC
AGCTCCCCCTTTGAGTCGGTCTGTTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGC
CAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGCCCTGCTCAACAAGAACAACCCCAAGTTCCTG
GCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGT
GGGCCCCAGGCCCTCGTGCAGATCATGCGTAACTACGTTATTAAAGCTGCTC

SEQ ID NO:388

>G3_4_44_PCR_G3F1 Direction: N/A

TCCAGTGCTGTGCTGGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCAC
AACCTCTCCACCACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTC
AGCTCCCCCTTGTGGAGTCTGTCTGTTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGC
CAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGCCCTGCTCAACAAGAACAACCCCAAGTTCCT
GGCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGG
TGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACTACGTTATGAAAAGCTGCTCTGGACCACCAGTCGTGTGCTC
AAGGTGCTATCCGTGTGTCCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGCAGGCCCTGGGCAAGCAC
CTGACCAGCAACAGCCCCCGCCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAGATTTGGCCACCAGG
CAGGAGGGC

SEQ ID NO:389

>G3_4_90_PCR_G3F1 Direction: N/A

CCAGTGCTGTGCTGGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCACA
ACCTCTCCACCACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTCA
GCTCCCCCTGTGGGAGTCGGTCTGTTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCC
AAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGCCCTGCTCAACAAGAACAACCCCAAGTTCCTG
GCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGT
GGGCCCCAGGCCCTCGTGCAGATCATGCGTAACTACAGTTATGAAAAGCTGCTCTGGACCACCAGTCGTGTGCTC
AAGGTGCTATCCGTGTGTCCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGCAGGCCCTGGGCAAGCAC
CTGACCAGCAACAGCCCCCGCCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAGATTTGGCCACCAGG

SEQ ID NO:390

>G3_5_91_PCR_G3F1 Direction: N/A

TGCTGTGCTGCTGCTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCACAACCT
CTCCACCACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTCAGCTC
CCCTTGGAGTCGGTCTGTTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATG
GCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGCCCTGCTCAACAAGAACAACCCCAAGTTCCTGGCCATC
ACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGTGGGCCC
CAGGCCCTCGTGCAGATCATGCGTAACTACAGTTATGAAAAGCTGCTCTGGACCACCAGTCGTGTGCTCAAGGTG
CTATCCGTGTGTCCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGCAGGCCCTGGGCAAGCACCTACCA
GCAACAGCCCCCGCCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAGATTTGGCCACCAGGAGGAGG
GCCTGGAGAGTGTGCTGAAAGATTCTGGTGA

SEQ ID NO:391

>G3_7_64_PCR_G3F1 Direction: N/A

AGCTTTTTTATAACTGTAGTTACGCATGATCTGCACGAGGGCCTGGGGCCACCATTGGCCAGGATGATCAGCTTG
CTCTCCTGGTTGCCGTAGCCAGAGCTGCAGCAGTCGTGTATGCCAGAACTTGGGGTTGTTCTTGTGAGCAGGGG
CACCATCTTTTGAGCCCGTCGCCAGGCGCACGGCCATCTTGGCGCCCTCCTGGTACAGGAGCAGGTTGTGCAGC
GTGGTGATGCATAGAACAGGACCGACTCCACANGGAGCTGAGCATGCGGACCAGAGCAGGATGCCACCACTTG

AAATGCAGCAGCCCCCTCCCGGTGTGGAGAGGTTGTGCAGGATGCTGTGGTGCAGCGGGCTGTGTCCAGTCGCTGT
ATTCTGCATGGTACGCACGACGCGCCACCCTGGGCGAGCCCATCAGGGCCCGCGACCCCTCCTTTTCGACGC
TGTTTACAATCATGCCCTTGTAC

5 SEQ ID NO:392

>GL1_34_HIGH_1_G3F1 Direction: N/A

10 GAGAGGCGCCATNGNCGGTGGCAGCGGTGGCTCCAGTGCTGTCGTGCGTACCATGCAGAATACCAGCGACCTGGA
CACAGCCCCGCTGCACCACCAGCATCCTGCACAACCTCTCCCACCACCGGGAGGGGCTGCTCGCCATCTTCAAGTC
GGGTGGCATCCCTGNTCTGTTACAGGAGGGCGCCAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTG
15 CTGCACAACCTGCTCCTGTACAGGAGGGCGCCAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTG
CCCCTGTCTCAACAAGAACAACCCCAAGTTCTTGGCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAAC
CAGGAGAGCAAGCTGATCATCCTGGCCAATGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTAT
GAAAAGCTGCTCTGGACCACCAGTCGTGTGCTCAAGGTGCTATCCGTGTGTCCAGCAATAAGCCTGCCATTGTG
15 GAGGCTGGTGGGATGCAGGCCCTGGGCAAGCACCTGACCAGCAACAGCCCCCGCCTGGTGCAGAACTGCCTGTGG
ACCTGCGCAACCTCTCAGATGTGGCCACCAGGCAGGAGGGCCTGGAG

SEQ ID NO:393

>GL1_34_HIGH_2_G3F1 Direction: N/A

20 GNCGGTGGCAGCGGTGGCTCCAGTGCTGTCGTGCGTACCATGCAGAATACCAGCGACCTGGACACAGCCCCGCTGC
ACCACCAGCATCCTTGCACAACCTCCCCACCACCGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCT
GCTCTGGTCCGATGCTCAGCTCCCCCTGNTGGAGTCGGTCCGACGGGCTGCAAAAGATGGTGCCCCCTGCTCAACAA
CCTGTACAGGAGGGCGCCAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGCCCCCTGCTCAACAA
25 GAACAACCCCAAGTTCTTGGCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACAGGAGAGCAAGCT
GATCATCCTGGCCAATGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTATGAAAAGCTGCTCTG
GACCACCAGTCGTGTGCTCAAGGTGCTATCCGTGTGTCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGAT
GCAGGCCCTGGGCAAGCACCTGACCAGCAACAGCCCCCGCCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCT
CTCAGATGTGGCCACCAAGCAGGAGGGCCTGGAGAGTGTGCTGAAGATTCTGGTGAATCAGCTGAGTGTGGATGA
CGTCAACGTCCTCACCCTGTGCCACGGGCACACTCTCCAACCTGACATGCAACAACAGCAAGAACAAGACGCTGGT
30 GACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGTGTGGTGACAAGGACGACATCACGGAGCC
TGCCGCTGCGCTCTGCGCCACCTCACTAGCCGNCACCTGAGGNCGAGAACGGCCTGGCCCCAGTAACGGGCCC
CTCTNTGCAGGCTTCTCTCTCTCTAGAACCTCCTTCTGTTGGAAGGCCCTCCG

SEQ ID NO:394

>GL1_34_HIGH_3_G3F1 Direction: N/A

35 GAGAGGCGCCATNGNCGGTGGCAGCGGTGGCTCCAGTGCTGTCGTGCGTACCATGCAGAATACCAGCGACCTGGA
CACAGCCCCGCTGCACCACCAGCATCCTGCACAACCTCTCCCACCACCGGGAGGGGCTGCTCGCCATCTTCAAGTC
GGGTGGCATCCCTGCTCTGGTCCGATGCTCAGCTCCCCCTGATGGAGTCGGTCCTGTTCTATGCCATCACCACGC
TGCACAACCTGCTCCTGTACAGGAGGGCGCCAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTG
40 CCTGCTCAACAAGAACAACCCCAAGTTCTTGGCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACC
AGGAGAGCAAGCTGATCATCCTGGCCAATGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTATG
AAAAGCTGCTCTGGACCACCAGTCGTGTGCTCAAGGTGCTATCCGTGTGTCCAGCAATAAGCCTGCCATTGTGG
AGGCTGGTGGGATGCAGGCCCTGGGCAAGCACCTGACCAGCAACAGCCCCCGCCTGGTGCAGAACTGCCTGTGGA
CCCTGCGCAACCTCTCAGATGTGGCCACCAAGCAGGAGGGCCTGGAGAGTGTGCTGAAGATTCTGGTGAATCAGC
TGAGTGTGGATGACGTCAACGTCCTCACCCTGTGCCACGGGCACACTCTCCAACCTGACATGCAACAACAGCAAGA
45 ACAAGACGCTGGTGACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGTGTGGTGACAAGGACG
ACATCACGGAGCCTGCCGCTGCGCTCTGNGCCANCTCATTAGCCGCCACCCTGAGGGCGAGATGGNCCAGAACT
CTGTGCGTCNCAACTATGGCATCCCA

SEQ ID NO:395

>GL3_1.36_A3_M13F Direction: N/A

50 TGGTGGTCCAGAGCAGCTTTTTATAACTGTAGTTACGCATGATCTGCACGAGGGCCTGGGGCCACCATTGGCCA
GGATGATCAGCTTGCTCTCTGGTTGCCGTAGGCCAGGAGCTGNAGGCAGTCGGTGGTGATGGCCANGAACTTGG
GGTTGNTCTTGTGAGCAGGGGCACCATCTTTTGCAGCCCGTCGGCCAGGCGCACGGCCATCTTGGCGCCCTCCT
GGTACAGGAGCAGGTTGTGACGCGTGGTGTATGGCATAGAACAGGACCGACTCCACAGGGGAGCTGATCATGCGGA
55 CCAGAGCAGGGATGCCACCCGACTTGAAGATGGCGAGCAGCCCTCCCGGTGGTGGGAGAGGTTGTGCAGGATGC
TGGTGGTGCAGCGGGCTGTGTCCAGGTCGCTGGTATTCTGCATGGTACGCACGACAGCGGCCACCAGCTGGGGCG
AGCCCATCANGGCCCGNCGGACGCGCTCCTTGTTCGACAGCTGGTCCACAATCATGGCCGNCTTGGTCAACACCA
CCGGGTCTCTG

SEQ ID NO:396

>GL3_1.36_A3_M13R Direction: anti-sense

CGGNCCGACCCCGACCCGGCCCGGTGAGGCCCATCTAGTAGCCACGATGGAGGTGATGAACCTGATGGAGCA
5 GCCTATCAAGGTGACTGANTGGCAGCAGACATACACCTACGACTCGGGTATCCACTCGGGCGCCAAACACCTGCGT
GCCCTCCGNCAGCAGCAAGGGCATCATGGAGGAGGATGAGGCCTGCGGGCGCCAGTACACGCTCAAGAAAACAC
CACTTACACCCAGGGGGTGGCCCCCAGCCAAGGTGACCTGGAGTACCAGATGTCCACAACAGCCAGGGCCAAACG
GGTGCGGGAGGCCATGTGCCCTGGTGTGTGTCAGGCGAGGACAGCTCGCTTCTGCTGGCCACCAGGTGGAGGGGCA
GGCCACCAACCTGCAGCGACTGGCCGAGCCGTCCCAGCTGCTCAAGTCGGCCATGTGTGCATCTCATCAACTACCA
10 GGACGATGCCGAGCTGGCCACTCGCGCCCTGCCCCGAGCTCACCAAACTGCTCAACGACGAGGACCCGGTGGTGGT
GACCAAGGCGGNCATGATTGTGAACAGCTGTGCAACAAGGAGGCGTCGCGGCGGGCCCTGATGGGCTCGCCCCA
GCTGGTGGCCGCTGTGTCGTGCGTACCATGCAGAATAACAGCGACCTGGACACAGCCCGCTGCACCACAGCATCCT
GCACAACCTCTCCACCACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGNATCCCTGTCTGGTCCGCAT
GCTCAGCTCCCTGTGGAGTCGGTCTGTCTATGCCATCACCACTGNACAACCTGCTCCTGTACCAGGAGGGGC
15 GCCAANATGGCCGTGCGCCTGGCCGACGNTGGAAAANATGTGCCCTGCTCAACAGAACACCCCAAGTTCTGGCA
TCACACGAAT

SEQ ID NO:397

>GL3_10.28_PCR_G3F1 Direction: N/A

NGGTGGTCCAGANCAGCTTTTTATAACTGTAGTTACGCATGATCTGCACNAGGGCCTGGGGCCCACCATATGGCC
20 AGGATGATCAGCTTGCTCTCCTGGTTGCCGTAGGCCAGGAGCTGCAGGCAGTCCGGTGGTGGTGGCCAGGAACCTTG
GGGTTGTTCTTGTGAGCAGGGGCACCATCTTTGTCAGCCCGTCGGCCAGGCGCACGGCCATCTTGGCGCCCTCC
TGGTACAGGAGCAGGTTGTGTCAGCGTGGTGGATGGCATAGAACAGGACCGACTCCACAGGGGAGCTGAGCATGCGG
ACCAGAGCAGGGATGCCACCCGACTTGAANATGGCGAGCAGCCCTCCCGGTGGTGGGAGAGGTTGTGTCAGGATG
25 CTGGTGGTGCAGCGGGCTGTGTCCAGGTGCTGGTATTCTGCATGGTACGCACGACAGCGGCCACCAGCTGGGGC
GAGCCCATCAGGGNCCCGCGGACGCCTCCTTGTTCGACAGCTGGTTCACAATCATGGCCGCCTTGGTCACCAC
CACCGGGT

SEQ ID NO:398

>GL3_9.60_PCR_G3F1 Direction: N/A

TGGTGGTCCAGAGCAGCTTTTTATAACTGTAGTTACGCATGATCTGCACGAGGGCCTGGGGCCCACCATTTGGCCA
30 GGATGATCAGCTTGCTCTCCTGGTTGCCGTAGGCCAGGAGCTGCAGGCAGTCCGGTGGTGGTGGCCAGGAACCTTGG
GGTTGTTCTTGTGAGCAGGGGCACCATCTTTGTCAGCCCGTCGGCCAGGCGCACGGCCATCTTGGCGCCCTCCT
GGTACAGGAGCAGGTTGTGTCAGCGTGGTGGATGGCATAGAACAGGACCGACTCCACAGGGGAGCTGAGCATGCGGA
CCAGAGCAGGGATGCCACCCGACTTGAAGATGGCGAGCAGCCCTCCCGGTGGTGGGAGAGGTTGTGTCAGGATGC
35 TGGTGGTGCAGCGGGCTGTGTCCAGGTGCTGGTATTCTGCATGGTACGCACGACAGCGGCCACCAGCTGGGGCG
AGCCCATCAGGGCCCGCGCGACGCCTCCTTGTTCGACAGCTGGTTCACAATCATGGCCGCCTTGGTCACCACCA
CCGGGTCTCTGTCGTTGAGCAGTTTGGTGAGCTCGGGCAGGGCGCGAGTGGCCAGCTCGGCATCGTCTCTGGTAGT
TGATGAGATGCACAATGGCCGACTTGAGCAGCTGGGACGGCTCGGCCAGTCGCTGCAGGTTGGTGGCCTGCCCT
CCACCTGGGTGGCCAGCAGAAGCGAGCTGTCTCGCCTGACACACCAGGGGCACATGGCCTCCCGCACCCGTTTGG
40 CCCTGGCTGTTGTGGACATCTGGTACTCCAGGTACCTTGGCTTGGGGGGCACCCCTGGGTGTAAGTGGTGGTT
TTCTTGAGCGTGTACTGGCGCCCGCAGGCCTCATCTCTCCATGATGCCCTTGTGC

SEQ ID NO:399

>GL3_9.66_PCR_G3F1 Direction: N/A

TGGTGGTCCAGAGCAGCTTTTTATAACTGTAGTTACGCATGATCTGCACGAGGGCCTGGGGCCCACCATTTGGCCA
45 GGATGATCAGCTTGCTCTCCTGGTTGCCGTAGGCCAGGAGCTGCAGGCAGTCCGGTGGTGGTGGCCAGGAACCTTGG
GGTTGTTCTTGTGAGCAGGGGCACCATCTTTTTCAGCCCGTCGGCCAGGCGCACGGCCATCTTGGCGCCCTCCT
GGTACAGGAGCAGGTTGTGTCAGCGTGGTGGATGGCATAGAACAGGACCGACTCCACAGGGGAGCTGAGCATGCGGA
CCAGAGCAGGGATGCCACCCGACTTGAAGATGGCGAGCAGCCCTCCCGGTGGTGGGAGAGGTTGTGTCAGGATGC
50 TGGTGGTGCAGCGGGCTGTGTCCAGGTGCTGGTATTCTGCATGGTACGCACGACAGCGGCCACCAGCTGGGGCG
AGCCCATCAGGGCCCGCGCGACGCCTCCTTGTTCGACAGCTGGTTCACAATCATGGCCGCCTTGGTCACCACCA
CCGGGTCTCTGTCGTTGAGCAGTTTGGTGAGCTCGGGCAGGGCGCGAGTGGCCAGCTCGGCATCGTCTCTGGTAGT
TGATGAGATGCACAATGGCCGACTTGAGCAGCTGGGACGGCTCGGCCAGTCGCTGCAGGTTGGTGGCCTGCCCT
CCACCTGGGTGGCCAGCAGAAGCGAGCTGTCTCGCCTGACACACCAGGGGCACATGGCCTCCCGCACCCGTTTGG
55 CCCTGGCTGTTGTGGACATCTGG

SEQ ID NO:400

>GL3_9.94_PCR_G3F1 Direction: N/A

TGGTGGTCCAGAGCAGCTTTTTATAACTGTAGTTACGCATGATCTGCACGAGGGCCTGGGGCCCACCATTTGGCCA
60 GGATGATCAGCTTGCTCTCCTGGTTGCCGTAGGCCAGGAGCTGCAGGCAGTCCGGTGGTGGTGGCCAGGAACCTTGG

GGTTGTTCTTGTGAGCAGGGGCACCATCTTTTGCAGCCCGTCGGCCAGGCGCACGGCCATCTTGGCGCCCTCCT
GGTACAGGAGCAGGTTGTGTCAGCGTGGTGATGGCATAGAACAGGACCGACTCCACAGGGGAGCTGAGCATGCGGA
CCAGAGCAGGGATGCCACCCGACTTGAAGATGGCGAGCAGCCCCCTCCCGGTGGTGGGAGAGGTTGTGTCAGGATGC
TGGTGGTGCAGCGGGCTGTGTCCAGGTGCTGCTGATTTCTGCATGGTACGCACGACAGCGGCCACCAGCTGGGGCG
AGCCCATCAGGGGCGCGCGACGCCCTCCTTGTTCGACAGCTGGTTTACAATCATGGCCGCCTTTGGTCAACCAC
CACCGGGTCCTCGTCTGTGAGCAGTTTGGTTAAGCTCGGGCAGGGCGCGAGTGGCCAGCTCGGCATCGTCTGTGT
AGTTGATGAGATGCACAA

SEQ ID NO:401

>GL1_34_HIGHPLKS_1 Direction: N/A

CANGAGAGCAAGCTGATCATCCTGGCCAATGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTAT
GAAAAGCTGCTCTGGACCACAGTCTGTGTCTCAAGGTGCTATCCGTGTGTCCCAGCAATAAGCCTGCCATTGTG
GAGGCTGGTGGGATGCAGGCCCTGGGCAAGCACCTGACCAGCAACAGCCCCGACCTGGTGCAGAACTGCCTGTG
GACCTTGCAGCAACCTCTCAGATGTGGCCACCAGGAGGAGGCTGGAGAGTGTGCTGAAGATTCTGGTGAATCA
GCTGAGTGTGGATGACGTCAACGTCCTCACCTGTGCCACGGGCACACTCTCCAACCTGACATGCAACAACAGCAA
GAACAAGACGCTGGTGCACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGTGTGGTGACAAGGA
CGACATCAGGGAGCTGCCGTCTGCGCTCTGCGCCACCTCACTAGCCGCCACCCTGAGGCCGAGATGGCCAGAA
CTCTGTGCGTCTCAACTATGGCATCCAGCCATCGTGAAGCTGCTCAACCAGCCCCAACCAGTGGCCACTGGTCAA
GGCAACCATCGGCTTGATCAGGAATCTGGCCCTGTGCCCCAGCCCCAACCATGCCCCGCTGCAGGAGGCAGNGGTC
ATCCCCGCTCGTCCAACCTGCTGGTGAANGCCCACAGGATGCCAGNGCCACGTANCTGCAGGCNACCAGCAGC

SEQ ID NO:402

>GL1_34_HIGHPLKS_2 Direction: N/A

CCCTGNATAATACNTTAGTGTGGATGACGTCAANGTCTCCTCNCTGCTGCCACGGGGACACTCTCCAACCTGACAT
GCAACAACAGCAAGAACAAGACGCTGGTGACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGAT
GCTGGTGACAAGGACGACATCACGGAGCCTGCCGTCTGCGCTCTGCGCCACCTCACTAGCCGCCACCCTGAGGCC
GAGATGGCCCCAGAACTCTGTGCGTCTCAACTATGGCATCCCAGCCATCGTGAAGCTGCTCAACCAGCCCCAACCAG
TGGCCACTGGTCAAGGCAACCATCGGCTTGATCAGGAATCTGGCCCTGTGCCAGCCAACCATGCCCCGCTGCAG
GAGGCAGCGGTCTATCCCCCGCTCGTCCAACCTGCTGGTGAAGGCCCCACAGGATGCCAGCGCCACGTAGCTGCA
GGCACACAGCAGCCCTACACGGATGGTGTGAGGATGGAGGAGATTGTGGAGGGCTGCACCGGAGCACTGCACATC
CTCGCCCCGGGACCCCATGAACCGCATGGAGATCTTCCGGCTCAACACCATTCCCCTGTGTGTCAGCTCCTGTAC
TCGTGCGTGGAGAACATCCAGCGCGTGGCTGCCGGGGTGTGTGTGAGCTGGCCCCAGGACAAGGAGGCGGTGCGAC
GCCATTGATGCAGANGGGGCTCGGCCCCACTCATGGAGTTGTGCACTCCCGCAACGAGGGCACTGCCACCTAC
GCTGCTGCCCCGTCTGTTCGCTATCTCCGANGACAANAACCCAGACTACCGGAANCGCGTGTCCGTGGAGCTCAC
CAACTCCCTTCTTCANGCATGAACCCGGCTGCC

SEQ ID NO:403

>GL1_34_HIGHPLKS_3 Direction: N/A

GCACACTGNACTGATCNGGTATCTGGCCCNNTGCCAGCCAACCATGCCCCGCTGCAGGAGGCAGCGGATCATCC
CCCCGCTCGCTCCAACCTGCTGGTGAAGGCCACCAGGATGCCAGCGCCACGCTAGCTGCAGGCACACAGCAGCC
CTACACGGATGGTGTGAGGATGGAGGAGATTGTGGAGGGCTGCACCGAGCACTGCACATCCTCGCCGGGACCC
CATGAACCGCATGGAGATCTTCCGGCTCAACACCATTCCCCTGNTTTGTGTCAGCTCCTGTACTCGTGGTGGAGA
ACATCCAGCGCGTGGCTGCCGGGGTGTGTGTGAGCTGGCCAGGACAAGGAGGCGGCCGACGCCATTGATGCAG
AGGGGGCCTCGGCCCACTCATGGAGTTGCTGCACTCCCGCAACGAGGGCACTGCCACCTACGCTGCTGCCGTCC
TGTTCGCTATCTCCGAGGACAAGAACCAGACTACCGGAAGCGCGTGTCCGTGGAGCTACCAACTCCCTCTTCA
AGCATGACCCGGCTGCCCTGGGAGGCTGCCAGAGCATGATTCCCATCAATGAGCCCTATGGAGATGACTNGGATG
CCACCTACCGCCCCATGTACTCCAGCGATGTGCCCTTGAACCCGCTGGAGATGCACATGGACATGGATGGAGAC
TACCCCATCGACACCTACAGNGANGGCCCTCAGGCCCCGTACCCCACTGNAGACCACATGCTGNNCTACCGGCC
TGGCCCCAGTACGGNCCCTCTTTGTCAGGCTTTTCTCCTCTCTAGAAACCTCCTTCTGTTGGAGGCCCTCNCAA
AACCANCAGNACAACCACACAGNGGTTACATAGATAAAGCGNCCGNTCGACTANTCTGAGGTCTGATACTCA
CTGACTGTCNTACACAGTGAACCTATAAANTAA

SEQ ID NO:404

>GL1_34_HIGHPLKS_4 Direction: sense

AACCTTNTGAATGNCGACCTTTGTGTGAGCTGGCCCAGGACAAGGCAGGCGGCCGACGCCATTGATGCANAGGG
GGCCTCGGCCCCACTCATGGAGTTGTGCACTCCCGCAACGAGGGCACTGCCACCTACGCTGCTGCCGTCTGTGT
CCGATCTCCGAGGACAAGAACCAGACTACCGGAAGCGCGTGTCCGTGGAGCTACCAACTCCCTCTTCAAGCA
TGACCCGGCTGCTGGGAGGCTGCCAGAGCATGATTCCCATCAATGAGCCCTATGGAGATGACTTGGATGCCAC
CTACCGCCCCATGTACTCCAGCGATGTGCCCTTGAACCGCTGGAGATGCACATGGACATGGATGGAGACTACCC

CATCGACACCTACAGCGACGGCCTCAGGCCCCCGTACCCCACTGCAGACCACATGCTGGCCTAGGCGGCCCTGGCC
CCAGTACGGCCCCCTCTTTGCAGGCTTTTCTCTCTCTAGAACCTCCTTCTGTTGGAGGCCCT

SEQ ID NO:405

5 >GL1_34_HIGH_1_G3R1 Direction: N/A
AGGGCCTCCAACAGAAGGAGGTTCTAGAGAGGAGGAAAAGCCTGCAAAGAGGGGGCCGTACTGGGGCCAGGCCGC
CTAGGCCANCATGTGGTCTGCAGTGGGGTACGGGGGCTGAGGCCGTGCTGTAGGTGTCGATGGGGTAGTCTCC
ATCCATGTCCATGTGCATCTCCAGNNGGTCAAGGGGCACATCGCTGGAGTACATGGGGCGGTAGGTGGCATCCAA
GTCATCTCCATAGGGCTCATTGATGGGAATC

SEQ ID NO:406

10 >gi|4504810|ref|NM_002230.1| Homo sapiens junction plakoglobin (JUP), ,
transcript variant 1, mRNA
CGCCAGAGTCCGGAGCAGCCCGCCCGACCGCGCCGAGCTCAGTTCGCTGTCCGCGCCGGCTCCACCCC
15 CGGCCCCGACCCCCGACCCGGCCCGGTCAGGCCCCATACTCAGTAGCCACGATGGAGGTGATGAACCTGATG
GAGCAGCCTATCAAGGTGACTGAGTGGCAGCAGACATACACCTACGACTCGGGTATCCACTCGGGCGCCA
ACACCTGCGTGCCCTCCGTCAGCAGCAAGGGCATCATGGAGGAGGATGAGGCCTGCGGGCGCCAGTACAC
GCTCAAGAAAACCACTTACACCCAGGGGGTGCCCCCAGCCAAGGTGACCTGGAGTACCAGATGTCC
20 ACAACAGCCAGGGCCAAACGGGTGCGGGAGGCCATGTGCCCTGGTGTGTGTCAGGCGAGGACAGCTCGCTTC
TGCTGGCCACCCAGGTGGAGGGGCGAGGCCACCAACCTGCAGCGACTGGCCGAGCCGTCCCAGCTGCTCAA
GTCGGCCATGTGTGCATCTCATCAACTACAGGAGGATGCCGAGCTGGCCACTCGCGCCCTGCCCCGAGCTC
ACCAAATGCTCAACGACGAGGACCCGGTGGTGGTGACCAAGGCGGCCATGATTGTGAACAGCTGTGCA
AGAAGGAGGCGTCGCGGCGGGCCCTGATGGGCTCGCCCCAGCTGGTGGCCGCTGTGCTGCGTACCATGCA
GAATACCAGCGACCTGGACACAGCCCGCTGCACCACAGCATCCTGCACAACCTCTCCACCACCGGGAG
25 GGGCTGCTCGCCATCTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTCAGCTCCCCTGTGGAGT
CGGTCTGTCTATGCCATCACCAGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCAAGATGGCCGT
GCGCCTGGCCGACGGGTGCAAAAGATGGTGGCCCTGCTCAACAAGAACAACCCCAAGTTTCTGGCCATC
ACCACCGACTGCTGTCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGTG
GGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTATGAAAAGCTGCTCTGGACCACAGCTCGTGT
30 GCTCAAGGTGCTATCCGTGTGTCCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGACGGCCCTG
GGCAAGCACCTGACCAGCAACAGCCCCCGCCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAG
ATGTGGCCACCAAGCAGGAGGGCCTGGAGAGTGTGCTGAAGATTCTGGTGAATCAGCTGAGTGTGGATGA
CGTCAACGTCTCACCTGTGCCACGGGCACACTCTCAACCTGACATGCAACAACAGCAAGAACAAGACG
CTGGTGACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGTGTGTTGACAAGGACGACA
35 TCACGGAGCCTGCCGTCTGCGCTCTGCCACCTCACTAGCCGCCACCCTGAGGCGGAGATGGCCAGAA
CTCTGTGCGTCTCAACTATGGCATCCCAGCCATCGTGAAGCTGCTCAACCAGCCCAACCAGTGGCCACTG
GTCAAGGCAACCATCGGCTTGATCAGGAATCTGGCCCTGTGCCAGCCAACCATGCCCCGCTGCAGGAGG
CAGCGGTTCATCCCCCGCCTCGTCCAATGCTGGTGAAGGCCACCAGGATGCCAGCGCCACGTAGCTGC
AGGCACACAGCAGCCCTACACGAGTGGTGTGAGGATGGAGGATTGTGGAGGGCTGCACCGGAGACTG
40 CACATCCTCGCCCCGGGACCCCATGAACCGCATGGAGATCTTCCGGCTCAACACCATTTCCCTGTGTTGTC
AGCTCCTGTACTCGTGGTGGAGAACATCCAGCGCGTGGCTGCCGGGGTGTGTGTGAGCTGGCCAGGA
CAAGGAGGCGGCCGACGCCATTGATGCAGAGGGGGCCTCGGCCCACTCATGGAGTTGCTGCACTCCCGC
AACGAGGGCACTGCCACCTACGCTGCTGCCGTCTGTTCCGCATCTCCGAGGACAAGAACCAGACTACC
GGAAGCGCGTGTCCGTGGAGCTACCAACTCCCTCTTCAAGCATGACCCGGCTGCCTGGGAGGCTGCCCA
45 GAGCATGATTCCCATCAATGAGCCCTATGGAGATGACATGGATGCCACCTACCGCCCCATGTACTCCAGC
GATGTGCCCTTGACCCGCTGGAGATGCACATGGACATGGATGGAGACTACCCCATCGACACCTACAGCG
ACGGCCTCAGGCCCCCGTACCCCACTGCAGACCACATGCTGGCCTAGGCGGCCCTGGCCCCAGTGACGGCC
CCCTCTTTGCAGGCTTTTCCCTCCTCTCTAGAACCTCCTTCTGTTGGAGGCCCTCCCATCTCCCCGCTGAA
ACCTGCGCTCCTTTTTTTGGGGGATCCTTTGCTGCTGAGCTTCCCCAAGCACGGTGTGCCCTGGCCTGCC
50 TTCTTCTGTGTCTTTGGTGGGGATGGGGAGGCCTATTCTGCTGGCCCCCTTCTGGGGGTGGTGGGCAGG
TGACACGGAGTGGCTTGAGCTTCTGGGGATGCAGGTCCACCGAGCCCCCTGACCCCTGTCTGTCCCCGCTC
CCCTAACAGGTGCGGTTCTCATCTGAGAGGCTCTCCGTGCAGGCGATGGGGCAAGACAGAAAAGTGCCT
GAGCTGGGGAAGCCGGGGTGTAACTTCTGCTGCACCTGCGCCTCCAGAGGTCTCCGTAGGGTCTTTTC
TTGGGATAGTGTCTGCTCCTGCTTTTCTGTCTGCTGGGCATGGGTCCAGGGCCCTGACACCCCTCCCCGCC
55 CCTGTGGCCCTGGCCACTAAAGCTTCAGACTCAAGTACCCATTCTGTTTTCCCCCAGCAACGCCCCCTCCA
AACCCTCAGCCTCCCTGTCTCCAGCTGCCTGGGCCCCGAAGGGCTTTGGTTCTTCTCTGTTGATTT
TCTCACTGAATCCACCGACCAACTGCCCTAAGCCCCAGGGCCTCCAGGGCCAGGTTCCGAGACCCAAA
CCCCCAAAATCCAAAATTTCTCTTGAAAAGTTCAAGGACCGTCCAGGGGAGATGGGGAGGAGATATGGAG
TGAGTCACTGCTCCAGAAGATGCCAGCTTCTCTCCAGGGTGTCTAGTTGGCTTTGCCCCACCCCTCAC
60 TCCCCAGGGAGCTCCGGGGACAGCTTCTCTCACACCCCTGTCCACCACACAGCTGCCCTAGCTGACCCC
GAGAAGTGCTCTTGGCTGACCCCTCTGGTGTGTGGTGGAGGGCTTTCTCTTCCCCTTCTGTTTCAGACC

CCCCATTTCCCGCACATGGTGTGGGGGGCTGGGGGAGGTCCAAGCAGAGTGTTTTATTATTATCGCTTT
ATGTTTTTGGTTATTGGTTTTTTTGTATAGACCAAAGCAAAGAAAATAAAAATAACACAG

SEQ ID NO:407

5 >gi|4504811|ref|NP_002221.1| junction plakoglobin, isoform 1; gamma-catenin
[Homo sapiens]

MEVMNLMEQPIKVTEWQQTYTYDSGIHSGANTCVPSVSSKGIMEEDEACGRQYTLKKTTTYTQGVPPSQG
DLEYQMSTTARAKRVREAMCPGVSGEDSSLLLATQVEGQATNLQRLAEPSQLLKSIVHLINQDDAELA
10 TRALPELTKLLNDEDPVVVTKAAMIVNQLSKKEASRRALMGSPQLVAAVVRTMQNTSDLDITARCTTSILH
NLSSHREGLLAIFKSGGIPALVRMLSSPVESVLFYAITTLHNLLLYQEGAKMAVRLADGLQKMPVLLNKN
NPKFLAITTDCLQLLAYGNQESKLIILANGGPQALVQIMRNYSYEKLLWTTSRVLKVLVSVCPSNKPATIVE
AGGMQALGKHLTSNSPRLVQNCWLTLRNLSDVATKQEGLESVLKILVNQLSVDDVNVLTCAATGTLNLT
NNSKNKTLVTQNSGVEALIHAILRAGDKDDITEPAVCALRHLTSRHPAEMAQNSVRLNYGIPAIKLLN
15 QPNQWPLVKATIGLIRNLALCPANHAPLQEA AVIPRLVQLLVKAHQDAQRHVAAGTQQPYTDGVRMEEIV
EGCTGALHILARDPMNRMEIFRLNTIPLFVQLLYSSVENIQRVAAGVLCELAQDKAADAIDAEGASAPL
MELLHSRNEGATATYAAAVLFRISEDKNPDYRKRVSVELTNSLKFKHPAAWEAAQSMIPINEPYGDDMDAT
YRPMYSSDVPLDPLEMHMDMDGDYPIDTYSGLRPPYPTADHMLA

SEQ ID NO:408

20 >gi|12056467|ref|NM_021991.1| Homo sapiens junction plakoglobin (JUP),
transcript variant 2, mRNA

CGCCAGAGTCCGGAGCAGCCGCCGCCGAGCTCAGTTTCGCTGTCCGCGCCGGCTCCCACCC
CGGCCCCGACCCGACCCGGCCCGGTGAGGCCCATCTAGTACGATGGAGGTGATGAACCTGATG
GAGCAGCCTATCAAGGTGACTGAGTGGCAGCAGACATACCTACGACTCGGGTATCCACTCGGGCGCCA
25 ACACCTGCGTGCCCTCCGTGAGCAGCAAGGGCATCATGGAGGAGGATGAGGCCTGCGGGCGCCAGTACAC
GCTCAAGAAAACCACTTACACCCAGGGGGTGCCTCCAGCCAAGGTGACCTGGAGTACCAGATGTCC
ACAACAGCCAGGGCCAAACGGGTGCGGGAGGCCATGTGCCCTGGTGTGTGAGGCGAGGACAGCTCGCTTC
TGCTGGCCACCCAGGTGGAGGGGCGAGGCCACCAACCTGCAGCGACTGGCCGAGCCGTCCACAGTCTCAA
GTGCGCCATTGTGTGATCTCATCTACCTACGAGCAGTACCGGAGCTGGCCACTCGCGCCCTGCCCGAGCTC
30 ACCAACTGCTCAACGACGAGGACCCGGTGGTGGTGACCAAGGCGGCCATGATTGTGAACAGCTGTGCA
AGAAGGAGGCGTTCGCGCGGGCCCTGATGGGCTCGCCCCAGCTGGTGGCCGCTGTGCTGCTACCATGCA
GAATACCAGCGACCTGGACACAGCCGCTGCACCAACAGCATCCTGCACAACCTCTCCCAACCCGAGG
GGGCTGTCTGCCATCTTCAAGTGGGTGGCATCCCTGCTCTGGTCCGATGCTCAGCTCCCCCTGTGGAGT
CGGTCTCTGTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATGGCCGT
35 GCGCCTGGCCGACGGGCTGCAAAAGATGGTGGCCCTGCTCAACAAGAACAACCCCAAGTTCCTGGCCATC
ACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACCAAGGAGAGCAAGCTGATCATCCTGGCCAATGGTG
GGCCCCAGGCCCTCGTGAGATCATGCGTAACCTACAGTTATGAAAAGCTGCTCTGGACCACCACTGCTGT
GCTCAAGGTGCTATCCGTGTGTCCTCCGATGAAGCTGCAAGATTCTGGTGAATCAGCTGAGTGTGAGTGA
40 GGCAAGCACCTGACCAGCAACAGCCCCGCTGGTGGTGCAAGCTGCCTGTGGACCCTGCGCAACCTCTCAG
ATGTGGCCACCAAGCAGGAGGGCCTGGAGAGTGTGCTGAAGATTCTGGTGAATCAGCTGAGTGTGAGTGA
CGTCAACGTCTCTACCTGTGCCACGGGCACACTCTCAACCTGACATGCAACAACAGCAAGAACAGACG
CTGGTGACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGTGTGGTGACAAGGACGACA
TCACGGAGCCTGCCGTCTGCGCTCTGCGCCACCTACTAGCCGCCACCCTGAGGCCGAGATGGCCAGAA
CTCTGTGCGTCTCAACTATGGCATCCCAGCCATCGTGAAGCTGCTCAACCAGCCCAACCACTGGCCACTG
45 GTCAAGGCAACCATCGGCTTGATCAGGAATCTGGCCCTGTGCCAGCCAACCATGCCCCGCTGAGGAGG
CAGCGGTATCCCCCGCTCGTCCAACCTGCTGGTGAAGGCCACCAGGATGCCAGCGCCACGTAAGTGC
AGGCACACAGCAGCCCTACACGGATGGTGTGAGGATGGAGGAGATTGTGGAGGGCTGCACCGGAGCACTG
CACATCTCGCCCGGGACCCCATGAACCGCATGGAGATCTTCCGGCTCAACACCATTCCTCTGTTGTG
AGCTCCTGTACTCGTGGTGGAGAACATCCAGCGCGTGGCTGCCGGGGTGTGTTGAGTGGAGTGGAGTGG
50 CAAGGAGGCGGCCGACGCCATTGATGCAGAGGGGGCTCGGCCCACTCATGGAGTTGCTGCACTCCCCG
AACGAGGGCACTGCCACCTACGCTGCTGCCGTCTGTTCCGATCTCCGAGGACAAGAACCAGACTACC
GGAAGCGCGTGTCCGTGGAGCTACCAACTCCCTCTTCAAGCATGACCCGGCTGCCTGGGAGGCTGCCCA
GAGCATGATTCCCATCAATGAGCCCTATGGAGATGACATGGATGCCACCTACCGCCCCATGTACTCCAGC
GATGTGCCCTTTGACCCGCTGGAGATGCACATGGACATGGATGGAGACTACCCCATCGACACCTACAGCG
55 ACGGCCTCAGGCCCGGTCACCCACTGCAGACACATGCTGGCCTAGGCGGCCTGGCCCCAGTGGCGTTC
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TGTAACCTTCTGCTGCACCTGCGCCTCCAGAGGCTCCTCCGTAGGGTCTTTCTTGGGATAGTGTCTGCT
CCTGCTTTTCTGTCTGGGATGGGTCCAGGGCCTGACACCCCTCCCCCGCTGTGGCCCTGAGGCACT
AAAGCTTCAGACTCAAGTACCATCTGTTTTCCCCAGCAACGCCCTCCAAACCTCCAGCCTCCCTGT
60 CTCCAGCTGCCTGGGCCCCGAAGGGCTTTGGTCTCTCTGCGGTCTGATTTTCTCACTGAACCTCACCG
ACCAACTGCCCTAAGCCCCAGGGCCTCCAGGGCCAGGTTGAGACCCAAACCCCAAAATCCAAACT

TCTCTTGAAAAGTTTCAGGGACCGTCCAGGGGAGATGGGGAGGAGATATGGAGTGAGTCACCTGCTCCAGA
AGATGCCAGCTTCTCTCTCCAGGGTGCTTAGTTGGCTTTGCCCCCCCCCTCACTCCCCAGGGAGCTCCGGG
GACAGCTTCTCCTCACACCCCTGTCCCACCCACACAGCTGCCCTAGCTGACCCCGAGAAGTGCTCTTGGCTG
ACCCCTCTGGTGTGTGGTGAGGGGCTTTCTCTTCCCTTCTCTGTTTCAGACCCCCCATTTCCCGCACAT
GGTGTGGGGGGCTGGGGGAGGTCCAAGCAGAGTGTPTTATTATTATCGCTTTATGTTTTTGGTTATTGGT
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SEQ ID NO:409

>gi|12056468|ref|NP_068831.1| junction plakoglobin, isoform 1; gamma-
catenin [Homo sapiens]
MEVMNLMEQPIKVTEWQQTYYTDSGIHSGANTCVPSVSSKGIMEEDEACGRQYTLKKTTTTYTQGVPPSQG
DLEYQMSTTARAKRVREAMCPGVSGEDSSILLATQVEGOATNLQRLAEPSSQLLSAIVHLINQDDAELA
TRALPELTKLLNDEDPVVVTKAAMIVNQLSKKEASRRALMGSPQLVAAVVRTMQNTSDLDTARCTTSILH
NLSSHREGLLAIFKSGGIPALVRMLSSPVESVLFYAITTLHNLLLYQEGAKMAVRLADGLQKMPVLLNKN
NPKFLAITTDCLQLLAYGNQESKLIILANGGPQALVQIMRNYSEKLLWTTSRVLKVLVSVCPNKAIVE
AGGMQALGKHLTSNSPRLVQNCLWTLRNLSDVATKQEGLESVLKILVNQLSVDDVNVLTCATGTLNLTLC
NNSKNKTLVTQNSGVEALIHAILRAGDKDDITEPAVCALRHLSRHPAEMAQNSVRLNYGIPAIVKLLN
QPNQWPLVKATIGLIRNLALCPANHAPLQEA AVIPRLVQLLVKAHQDAQRHVAAGTQQPYTDGVRMEEIV
EGCTGALHILARDPMNRMEIFRLNTIPLFVQLLYSSVENIQRVAAGVLCELAQDKEAADAIDAEGASAPL
MELLHSRNEGATATYAAAVLFRISEDKNPDYRKRVSVELTNSLKFHDPAAWEAAQSMIPINEPYGDDMDAT
YRPMYSSDVPLDPLEMHMDMDGDYPIDTYS DGLRPPYPTADHMLA

SEQ ID NO:410

Plasminogen activator inhibitor 1 (SERPINE1; PAI-1)

>GL3_6E_1_M13F Direction: N/A
AGGCANGNTACAAGTGTGATGGCAATGTGACTGGAAACAGAAATAGTTTCTATCCAGGCACATCAATAAGCTCCCT
GTAATGCCCCGTAGATTCCATCCTGCAAAAGTGGCCCTCAGTTGGCGACACCCACGTGTCTGCATGATCCCCGCA
GTTGTGTGCTACGCACGTAGGACGAGCGTTGGAATGCAAGGTTGCCCCANATCGGTCCCGCANGGCTTCACCGTC
TGGTTTGGATGACCTATCTAAGGGGAAGTTTCTGTGCTTCTAAACGATTCTTCTTCTCCAAAGGGTCTCAAGGGGT
CGGTAGACTATGGGAGCGATTTTGACCTTAAAGGTTTCTTCCCAAGNGAGAGAAGGGCCCAACGGGAGTCCT
TGGGACGAAGCGAGGGAGTCCTGTGCTTTTACTCAACATCTGTCTTAATCAATAGAGTGNCAAGATGCTCTATCG
TGCTTTCCCCTTCAGAGAAGTGAGGTTCAATTGTAACAGCATAAC

SEQ ID NO:411

>GL3_37G_PCR_G3F1 Direction: N/A

TCCGAGTTTCTTTCTTTCCCAGTGCATCTCCAGTTTGTGCCAGATGAAGGCGTCTTTCCCCAGGGTCAGGGGTTC
CATCACTTGGCCCATGAAAAGGACTGTTTCTGTGGGGTGTGCCGGAACAACAAAGAGGAAGGGTCTGTCCATGA
TGATCTCCTCGGGGGCCATGCGGGCTGAGACTATGACAGCTGTGGATGAGGAGGCCACCGTGCCACTCTCGTTCA
CCTCGATCTTCAGCTTTCTGCGAGCGCTGCGCGACGTGAGAGGCTCTTGGTCTGAAAGACTCGTGAAGTCAGCCTG
AAACTGTCTGAACATGTCGGTCAATCCAGGTTCTTAGGGGCTTCTGAGGTCGACTTCAGTCTCCAGGGAGAA
CTTGGGCAGAACAGGAGGCGGGGCGAGCTGTGTCATGTTGCTTCCAGTGGCTGATGAGCTGGGCACTCAGAAT
GTTGGTGAGGGCAGAGAGAGGCACCTCTTTTTCATAAGGGGCGAGCAATGAACATGCTGAGGGTGTCCCCGTGGTA
GGGCAGTTCAGGATGTCGTATAATGGCCATCGGGCGTGGTGAAC

SEQ ID NO:412

>GL3_6E_1_M13R Direction: anti-sense

GACACACACAAAAGGTATGATCAGCAACTTGCTTGGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGCTGGT
GAATGCCCTCTACTTCAACGGCCAGTGGAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCGCTCTTCCACAA
ATCAGACGGCAGCACTGTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAGTTACCACGCC
CGATGGCCATTACTACGACATCCTGGAAGTGCCTTACCACGGGGACACCCCTCAGCATGTTTATTGCTGCCCTTA
TGAAAAAGAGGTGCCTCTCTGTGCCCTCACCAACATTTCTGAGTGCCAGCTCCATCAAGCCACTGGAAGGCAAC
ATGACCAGGGGC

SEQ ID NO:413

>GL3_6E_2_M13F Direction: anti-sense

GACACACACAAAAGGTATGATCAGCAACTTGCTTGGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGCTGGT
GAATGCCCTCTACTTCAACGGCCAGTGGAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCGCTCTTCCACAA
ATCAGACGGCAGCACTGTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAGTTACCACGCC
CGATGGCCATTACTACGACATCCTGGAAGTGCCTTACCACGGGGACACCCCTCAGCATGTTTATTGCTGCCCTTA
TGAAAAAGAGGTGCCTCTCTGTGCCCTCACCAACATTTCTGAGTGCCAGCTCATCAGCCACTGGAAGGCAACAT

GACCAGGCTGCCCCGCTCCTGGTTCTGCCAAGTTCTCCCTGGAGACTGAAGTCGACCTCAGGAAGCCCCTAGA
GAACCTGGGAATGACCGACATGTTTCACTCTGTTTCAAGGCTGACTTCACGAGTCTTTCAGACCAAGAGCCTCTCC
ACGTCGCGCAGGCCTGAG

5 SEQ ID NO:414

>GL3_6E_3_M13F Direction: anti-sense

GACACACACAAAAGGTATGATCAGCAACTTGCTTGGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGCTGGT
GAATGCCCTCTACTTCAACGGCCAGTGGAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCCTCTTCCACAA
ATCAGACGGCAGCACTGTCTCTGTGCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAGGTTTACCACGC
10 CCGATGGCCATTACTACGACATCCCTGGAATGCCCTACCACGGGGACACCCTCAGCATGTTTCATTGCTGCCCCCT
T

SEQ ID NO:415

>GL3_36B_PCR_G3F1 Direction: N/A

15 AGGCAGTACAAGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTCCTGTAAGC
CCCGTAGTTCCATCCTGCAAAGGGCCTCAGTGGGAACCAGTCTTGGCAACCCATGGGCAGAGAGACGGGTGGAAG
CAGGTGCCCCAGATGGTCCCGCAGGCGTCACCGTCTGGTTTGGAGACCTTAAGGGAGTTGTGCTTCAAACCTCTC
TCCCAGGGGTCTCAGGTGGAGACTAGGGAGTTTGACCTAAAGGTCCTCCAAGGAGAGGCCAAGGTCTTGGAGACA
GATCTGGTTTACCATCTTTTAAACAAAAGGCAAATGTCTTCTTCTTCCCTCAGAAAGAGTCATTAACACTAAAATTC
20 TTTTCTTCGGAGTTTCTTCTTTCCCGATGCATCTCCAGTTTGTGCCAGATGAAGGCGTCTTTCCCCAGGGGTCA
GGGTTCCATCACTTGGCCCATGAAAAGGACTGTTCTGTGGGGTTGTGCCGGACCACAAAGAGG

SEQ ID NO:416

>GL3_6E_2_M13R Direction: sense

25 AGGCAGTACAAGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTCCTGTAAGC
CCCGTAGTTCCATCCTGCAAAGGGCCTCAGTGGGAACCAGGTCTGCAGACCCGAGTGGGCAGAGAGACGGGTGG
AAGCAGGTGCCCCAGATGGTCCCGCAGGCGTCACCGTCTGGTTTGGAGACCTTAAGGGAGTTGTGCTTCAAACCTT
CTCTCCCAGGGTCTCAGGTGGAGACTAGGGAGTTTGACCTAAAGGTCCTCCAAGGAGAGGCCAAGGTCTTGGAGA
CAGATCTGGTTTACCATCTTTTAAACAAAAGGCAAATGTCTTCTTCTTCCCTCAGAAAGAGTCATTAACACTAAAAT
30 TCTTTTCTTCGGAGTTTCTTCTTTCCCGATGCATCTCCAGTTTGT

SEQ ID NO:417

>GL3_6E_3_M13R Direction: sense

35 CAGCTGGANCGAGCTCGGATCACTTANTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTCTCTCGGCATGGACGA
GCTGTACAAGGAGGAGGCGCAAGGCCGGTGGCAGCGGTGGCTCCAGTGTGCTGGGTCTTGCAGAGGCAGTACA
AGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTCCTGTAAGCCCCGTAGTTC
CATCCTGCAAAGGGGCCCTCAGTGGGAACCAGGTCTGCAGACCCGAGTGGGCAGAGAGACGGGTGGAAGCAGGTGC
CCCAGATGGTCCCGCAGGCGTCACCGTCTGGTTTGGAGACCTTAAGGGAGTTGTGCTTCAAACCTTCTCTCCAGG
GTCTCAGGTGGAGACTAGGGAGTTTGACCTAAAGGTCCTCCAAGGAGAGGCCAAGGTCTTGGAGACAGATCTGGT
40 TTACCATCTTTTAAACAAAAGGCAAATGTCTTCTTCTTCCCTCAGAAAGAGTCATTAACACTAAAATTCCTTTCT

SEQ ID NO:418

>GL3_6E_PCR_G3F1 Direction: N/A

45 AGGCAGTACAAGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTCCTGTAAGC
CCCGTAGTTCCATCCTGCAAAGGGCCTCAGTGGGAACCAGGTCTGCAGACCCAGTGGGCAGAGAGACGGGTGGAA
GCAGGTGCCCCAGATGGTCCCGCAGGCGTCACCGTCTGGTTTGGAGACCTTAAGGGAGTTGTGCTTCAAACCTTCT
CTCCCAGGGTCTCAGGTGGAGACTAGGGAGTTTGACCTAAAGGTCCTCCAAGGAGAGGCCAAGGTCTTGGAGACA
GATCTGGTTTACCATCTTTTAAACAAAAGGCAAATGTCTTCTTCTTCCCTCAGAAAGAGTCATTAACACTAAAATTC
50 TTTTCTTCGGAGTTTCTTCTTTCCCGATGCATCTCCCGTTTGTGCCAGATAAGGCGTCTTTCCCCAGGGTCAGG
GTTTCCATCACTTGGCCCATGAAAAGGACTGTTCTCT

SEQ ID NO:419

>gi|10835158|ref|NM_000602.1| Homo sapiens serine (or cysteine) proteinase
inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member
1 (SERPINE1), mRNA

55 GAATTCCTGCAGCTCAGCAGCCGCCGCGCAGAGCAGGACGAACCGCCAATCGCAAGGCACCTCTGAGAACT
TCAGGATGCAGATGTCTCCAGCCCTCACCTGCCTAGTCTGGGCTGGCCCTTGTCTTTGGTGAAGGGTC
TGCTGTGCACCATCCCCATCCTACGTGGCCACCTGGCCTCAGACTTCGGGGTGAGGGTGTTCAGCAG
GTGGCGCAGGCCTCCAAGGACCGCAACGTGGTTTCTCACCTATGGGGTGGCCTCGGTGTTGGCCATGC
60 TCCAGCTGACAACAGGAGGAGAAACCCAGCAGCAGATTCAAGCAGCTATGGGATTCAAGATTGATGACAA

5 GGGCATGGCCCCCGCCCTCCGGCATCTGTACAAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGC
 ACCACAGACGCGATCTTCGTCCAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCACTTCTTCAGGC
 TGTTCGGGAGCACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCCAGATTTCATCATCAATGACTG
 10 GGTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGGAAAGGAGCCGTGGACCAGCTGACACGG
 CTGGTGCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTCCCCGACTCCAGCACCCACC
 GCCGCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAA
 CTATACTGAGTTCAACACGCCCGATGGCCATTACTACGACATCTTGGAACTGCCCTACCACGGGGACACC
 CTCAGCATGTTCAATGCTGCCCCCTTATGAAAAAGAGGTGCCCTCTCTCTGCCCTCACCAACATTCTGAGTG
 15 CCCAGCTCATCAGCCACTGGAAAGGCAACATGACCAGGTGCCCGCCCTCTGGTTCTGCCCAAGTTCTC
 CCTGGAGACTGAAGTCGACCTCAGGAAGCCCCCTAGAGAACCCTGGGAATGACCGACATGTTTCAGACAGTTT
 CAGGCTGACTTCACGAGTCTTTTCAGACCAAGAGCCTCTCCACGTGCGCGCAGGCGCTGCAGAAAGTGAAGA
 TCGAGGTGAACGAGAGTGGCAGGTGGCCTCCTCATCCACAGCTGTATAGTCTCAGCCCGCATGGCCCC
 CGAGGAGATCATATGGACAGACCCCTTCTCTTTGTGGTCCGGCACAACCCACAGGAACAGTCTTTTTC
 ATGGGCCAAGTGATGGAAACCTGACCTTGGGGAAAGACGCCCTTCATCTGGGACAAAACCTGGAGATGCATC
 20 GGGAAAGAAGAACTCCGAAGAAAAGAAATTTTAGTGTTAATGACTCTTTCTGAAGGAAGAGAAGACATTT
 GCCTTTTGTATAAAGATGGTAAACCAGATCTGTCTCCAAGACCTTGGCCTCTCTTGGAGGACCTTTAGG
 TCAAACCTCCCTAGTCTCCACCTGAGACCTTGGGAGAGAAGTTTGAAGCACAACCTCCCTTAAGGTCTCAA
 ACCAGACGGGTGACGCCCTGCGGGACCATCTGGGGACCTGCTTCCACCCGCTCTCTTGCCCACTCGGGTCT
 GCAGACCTGGTTCCCACTGAGGCCCTTTGCAGGATGGAACCTACGGGGCTTACAGGAGCTTTTGTGTGCCT
 25 GGTAGAAACTATTTCTGTTCCAGTCACATTGCCATCACTCTTGTACTGCCTGCCACCGCGGAGGAGGCTG
 GTGACAGGCCAAAGGCCAGTGAAGAAAACACCCCTTTTCATCTCAGAGTCCACTGTGGCACTGGCCACCCCT
 CCCAGTACAGGGGTGCTGCAGGTGGCAGAGTGAATGTCCCCCATCATGTGGCCCAACTCTCTCGGCCTG
 GCCATCTCCCTCCCCAGAAACAGTGTGCATGGGTATTTTGGAGTGTAGGTGACTTGTTTACTCATTGAA
 GCAGATTTCTGCTTCTTTATTTTATAGGAATAGAGGAAGAAATGTGAGATGCGTGCCAGCTCTTCA
 30 CCCCCAATCTCTTGGTGGGGAGGGGTGTACCTAAATATTTATCATATCCTTGGCCCTGAGTGCTTGT
 GAGAGAAAGAGAACTACTAAGGAAATAATATTATTAACCTCGCTCCTAGTGTCTTTTGTGGTCTGTG
 TCACCGTATCTCAGGAAGTCCAGCCACTTGACTGGCACACACCCCTCCGGACATCCAGCGTGACGGAGCC
 CACACTGCCACCTTGTGGCCGCTGAGACCTCGCGCCCCCGCGCCCCCGCGCCCTCTTTTCCCCCT
 TGATGGAAATGACCATACAATTTTCATCTCCTTTCAGGGGATCAAAGGACGGAGTGGGGGGACAGAGAC
 35 TCAGATGAGGACAGAGTGGTTTCCAATGTGTTCAATAGATTTAGGAGCAGAAATGCAAGGGGCTGCATGA
 CCTACCAGGACAGAACTTTCCCCAATTACAGGGTGAATCACAGCCGATTTGGTGAATCACTTCAATGTGT
 CATTTCCGGCTGCTGTGTGTGAGCAGTGGACACGTGAGGGGGGGGTGGGTGAGAGAGACAGGCAGCTCGG
 ATTCAACTACCTTAGATAATATTTCTGAAAACCTACCAGCCAGAGGGTAGGGCACAAGATGGATGTAAT
 GCACCTTTGGGAGGCCAAGGCGGAGGATGTCTTGAAGCCAGGAGTTCAAGACCAGCTGGGCAACATACC
 40 AAGACCCCGTCTCTTTTAAATAATATATATATTTTAAATATATCTTAAATATCTTTAA
 TATATATATATATTTTAAAGACCAATTTATGGGAGAATTGCACACAGATGTGAAATGAATGTAATCTAAT
 AGAAGC

SEQ ID NO:420

40 >gi|10835159|ref|NP_000593.1| serine (or cysteine) proteinase inhibitor,
 clade E (nexin, plasminogen activator inhibitor type 1), member 1;
 plasminogen activator inhibitor, type I [Homo sapiens]
 MQMSPALTCLVLGLALVFGEESAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSFYGVASVLAAMLQ
 45 LTTGGETQQQIQAMGFKIDDKGMALRHLKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLF
 RSTVKQVDFSEVERARFIINDWVKHTKGMISNLLGKGAVDQLTRLVLVNLALYFNGQWKTPFPDSSTHRR
 LFHKSDGSTVSVPMMAQTNKFNTEFTTPDGHYDILELPYHGDLSMFIAAPYEKEVPLSALTNILSAQ
 LISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIE
 VNESGTVASSSTAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP

50 SEQ ID NO:421

Proteosomal subunit Y>

AACTGCCCCCTCTTCTTGGGGTCCCAGCCTGCGATGATGATTCGCCCATCAGGTCTTCCCGGTATCGGTAAACA
 CATCTCCTTAAAGAGACTGGCTGCTGTGTGGACCAGTGGAGGCTCATTCACTTCAATGCTGTGGAAACCGAGCTG
 55 GTAGGTGACAGCATCAGTACTGCCTGGGTATCAGCAGCTGAGCCTGAGCGACAGCAGAAAATGCGGTGCTGAAT
 AGGTGTGCTGTGCTGACTCGATTGGCGATGTAGGACCCAGTGGTTGTCTTGGAGTCCGCCCCCAGAACCCAC
 GCCCCCTCAAACCTGCACGGCATGATAGTCCCGGAACTTCTCGGCTTTCCAGTCTGGAGTGAACGC
 CTCCGGCCCCCAAGCCGGTGTGGCCCGGCTCCCCGAGCAGCTAGTAAGGTAG

SEQ ID NO:422

Rap2B

>GL3_37F_1_M13F Direction: N/A

5 CGAACTGCTCGGTGCCCCGCGTATCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTACTTCTCGATGAAGGAGCCCGTCACGAACTGCACGGTGAGCGCGGACTTGCC
CCACGCCGCCCGAGCCCGAGCACCACCACTTTGTACTCTCTCATGGCTCCGTTCAGCGCTCTCGCCGCGCCTGCCGC
GGCCCCGTTCGGGGCTGCGCGCGGGGAAAGGCTGGGCTTGGCGGGCTGGACTTCTCTTCCCCCTTCCTCAGCTACGCA
GGAAAAACCCAGGAGAGAGCAACCCAGAGAACGCAGGGCGGAAACCACCGAAACGGAAGGCGGGCCGCCAGGCCCC
10 GGCCCGGCGGGCGGGCGGGCAAGGCGNTAATCCCTGGGGGCTAGCACGGGGTCCCGGGGGCCACGGAAGGCAAGG
TCACCGGNAGGCAGGCAAGGACANGACAGCCCCNGGNGGACGGGCGAGAAACCCGGGAANGAGGGGACAAATTGG
CCACGCGCAAGCCTTTGGCGNCACGNGAAGAAAAACCAAGGGCAACAAGGGGGNGTTAACGNCATTAAGGAA
TAACACAGCGCGGAGCCGAGAG

SEQ ID NO:423

15 >GL3_37F_4_M13F Direction: anti-sense

CGCAGCTGCGGGCATTTGTCTCTCGGTTTCGCCGCCCGGGCTGCTGCTGCCGCCCGGGACTGCTGCGGGGCCCCGGA
CCCCGACCCCCAGGGATACGCTGCCGCCCGTCCGCCGCCCGGGCCCGGCCCTCCGTTCCGTTGGTTTCCGCCCTG
CGTTCTCTGGGTTGCTCTCTCTCGGTTTTCCTGCGTAGCTGAGGAAGGGGAAGAGAAGTCCAGCCGCCAAGCC
20 CAGCCTTCCCCCGGCGCAGCCCCGACGGGGCCCGCGACAGGCGCGGGCGGAGAAGCGCTGACGGAGCCATGAGGA
GAGTACACAAGTGGTGGTGTAGGGCTCGAGGCAGGAGTGGGGCAAAGTCCGCAGACTTCAACCGTGGCAAGATA
CGGTTGGAACACGGGGCATCTTCAATCGNAGAAAGGTACGAACCCGAACNCATCGAAAGAAGCTTTTAAACCGG
CCAAGGNAGNAATGGAGAGTGGGACCTCAGGNCCTACGNCCCGTCCCGGGANGCTTGGAAGAATCC

SEQ ID NO:424

25 >GL3_37F_2_M13R Direction: sense

CGAACTGCTCGGTGCCCCGCGTATCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTACTTCTCGATGAAGGAGCCCGTCACGAACTGCACGGTGAGCAGCGGACTT
GCCCANAGACCCGACCGAGCCCGAGACACACACCACTATATGTACTCATCTCAATGGCATCCGNCAGAGCTCATCG
30 NCCGACAGACCTGCCGNGGACCCCGATACAGGGGGGCATTCAGCGCGGNGGAAAAGGGCATNGGGGNCATAGG
ACAGGGACAATAGGGAACAGNTATCATCATTCACACACATATCGCATCAAAGCNATACGCAAAGGGAAAAACAAN
AACGCCCAAGAGAAGAAAGAGGCAAAACCCCAAGGAANNGAAAACAACAGGGCCAACAAGAGGGGACCGGGGAG
GAAAAAAA

SEQ ID NO:425

35 >GL3_37F_3_M13F Direction: N/A

CGAACTGCTCGGTGCCCCGCGTATCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTACTTCTCGATGAAGGAGCCCGTCACGAACTGCACGGTGAGCGCGGACTTGCC
CCACGCCGCCCGAGCCCGAGCACCACCACTTTGTACTCTCTCATGGCTCCGTTCAGCGCTCTCGCCGCGCCTGCCGC
40 GGCCCCGTTCGGGGCTGCGCGCGGGGAAAGGCTGGGCTTGGCAGGCTGGACTTCTCTTCCCCCTTCCTCAGCTACGCA
GGAAAAACCCAGGAGAGAGCAACCCAGAGAACGCAGGGCGGGAAACCACCGAACGGAGGCCGGGCGCCGGGCCGT
CCGGCCCGACGANGGCAGTGCGGGGGCGAACCGAGAGGAACAAATGCCGAGAGGCCCTTGCGGCCGAAAAA

SEQ ID NO:426

45 >GL3_37F_4_M13R Direction: sense

CGAACTGCTCGGTGCCCCGCGTATCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTACTTCTCGATGAAGGAGCCCGTCACGAACTGCACGGTGAGCGCGGACTTGCC
CCACGCCGCCCGAGCCCGAGCACCACCACTTTGTACTCTCTCATGGCTCCGTTCAGCGCTCTCGCCGCGCCTGCCGN
GGCCCCGTTCGGGGCTGCGCGCGGGGAAAGGCTGGGCTTGGCGGCTGGACTTCTCTTCCCCCTTCCTCAGNTACGAG
50 GAAAAACCCAGGAGGAGAGCAACCCAGGAGAACGCAGGGCGGAAAGCACGCGGAACGGAGTGCCGGGCGCCGGGC
CGGCCCG

SEQ ID NO:427

55 >GL3_37F_PCR_G3F1 Direction: sense

CGAACTGCTCGGTGCCCCGCGTATCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTACTTCTCGATGAAGGAGCCCGTCACGAACTGCACGGTGAGCGCGGACTTGCC
CCACGCCGCCCGAGCCCGAGCACCACCACTTTGTACTCTCTCATGGCTCCGTTCAGCGCTCTCGCCGCGCCTGCCGC
GGCCCCGTTCGGGGCTGCGCGCGGGGAAAGGCTGGGCTTGGCGGCTGGACTTCTCTTCCCCCTTCCTCAGCTACGAG
GAAAAACCCAGGAGAGAGCAACCCAGAGAACGCAGGGCGGAAACCACCGAACGGAGGCCGGGCGCCGGGCCGGCC
GGCGGCGGCGGCAGCGTATCCCTGGGGTGCGGGTCCGGGCCCGCAGCAGTCCGCGGCGGCAGCAGACCCGGG

CGGCGAACCGAGAGGACAATGCCCCGAGCCTGCGCCGAGAACCCAGCACAGTGGTTAGATAGATAAAGCGGCGC
TCGACTAGTCTGAGGTCTGATACTCACTGACTGAA

SEQ ID NO:428

5 >gi|16159529|ref|XM_003032.2| Homo sapiens RAP2B, member of RAS oncogene
family (RAP2B), mRNA
GCACGTTCCGCGGGGACTCATGCCACGCGCGTCCCGGCCCCGACGCGCAATTAGCAGCCACCTCCGCAGCC
CGCCGCCACCGCCTCCCTGCCCTCCCGGGCTGCCGAGCTAGGAGCTCCAGCCGTGCGCTCGCGCAGGCT
10 GCGGGCATTGTCTCTCGGTTCCGCGCCCGGGCTGCTGCTGCCGCGCGGACTGCTGCGGGGCCCGGACC
CGCACCCAGGGATAACGCTGCCGCGCCCGGGCTGCTGCTGCCGCGCGGCTCCGTTCCGGTGGTTTCCGC
CCTGCGTTCTCTGGGTTGCTCTCTCTGCGTTTTCCTGCGTAGCTAGGAAGGGGAAGAGAAGTCCAGC
CGCCAAGCCCAGCCTTCCCGGCGCGCAGCCCCGACGGGGCCGCGGCAGGCGCGGCGAGAGCGCTGACGG
AGCCATGAGAGAGTACAAAGTGGTGGTGTGCTGGGCTCGGGCGCGTGGGCAAGTCCGCGCTCACCGTGCAG
15 TTCGTGACGGGCTCCTTCATCGAGAAGTACGACCCGACCATCGAAGACTTTTACCAGCAAGGAGATTGAGG
TGGACTCGTCGCGTCCGTGCTGGAGATCCTGGATACGGCGGGCACCAGCAGTTCGCGTCCATGCGGGA
CCTGTACATCAAGAACGGCCAGGGCTTCATCCTGGTCTACAGCCTCGTCAACCAGCAGAGCTTCCAGGAC
ATCAAGCCCATGCGGGACAGATCATCCGCGTGAAGCGGTACGAGCGCGTGGCCATGATCCTGGTGGGCA
ACAAGGTGGACCTGGAGGGTGAGCGCGAGGTCTCGTACGGGGAGGGCAAGGCCCTGGCTGAGGAGTGGAG
20 CTGCCCCCTTCATGGAGACGTGCGCCAAAAACAAGCCTCGGTAGACGAGCTATTTGCCGAGATCGTGCGG
CAGATGAACTACGCGCGCAGCCCCAACGGCGATGAGGGCTGCTGCTCGGCCTGCGTGATCCTCTGAGCGG
GCCACCGCGCGCCCGCGCGCTCTGCGCACAAAAGCCAAACGCATCCGACTCTCTAAATGTGATTTATTT
CTTGCTTTGAGATTGGAGACCACTTTGCATTGGCCAGGGTGTCTTGGGAGCCCGGCTGGCCTCCGCGGCC
GGCGTCCCCTGCCTCCACCCTGTGCCCGAGGGGGTGTCCGGTCTGCCCATCCGATACTCTGGTGGAAAT
25 GTGGCTCTTTGACAGATGTACGTTTCTCCCTGATTTTGGTTGATGCATATTTCCCGTTTAAGTAGCCGT
TAGGGCGCAGTATCGGCAGCTTGACACCCACCAAGCAAAAGTTTTCAGCCTGGAAAAAAATGGGGGGGAA
GGGTGGATGAAAAGGAGGGAGAGAAGGTGGAAATGGTTTTTTTTTTTTTTTTCTATTTTCTTTCTTTTT
TTTTTTTTTTTTTTTTTGGTCAACAGCCGTTTTTCTAGTTCCAAGTTTTAAATACATGGAAGGAAGTCCGG
GAGAACCATATGAAGGAGCAGGAGGAGAGGAAGAACTTTTTTCTTTTCCAGGAGTAGCTGGAAA
TTAAGATCGGGTTCTTTTCTGCCAGCTTGGAAAGGGCAACCCCATGACTGATTGCGATTCTGAGGATGTC
30 TATGCAAAGTTGGATTCTTGTACAGTGTATCCAATCTGAAGTATTGCACATCTGAACCTGGGACTGTAA
CACTGATGCCAATACAGTGTGGGGTGCCAGAAAGTGTCTGCTGATATTTGTGG

SEQ ID NO:429

35 >gi|11433346|ref|XP_003032.1| RAP2B, member of RAS oncogene family [Homo
sapiens]
MREYKVVVLGSGGVGKSALTVOFVTGSFIEKYDPTIEDFYRKEIEVDSSPSVLEILDITAGTEQFASMRDL
YIKNGQGFILVYSLVNQSFQDIKPMRDQIIRVKRYERVPMLVGNKVDLEGEREVSYGEGKALAEWESC
PFMETSANKASVDELFAEIVRQMNYYAQPNGDEGCCSACVIL

40 SEQ ID NO:430

Semaphorin 3F

>GL3_10.20_A_M13F Direction: anti-sense

CGGCAGAAAACAGAGCCTGCCTAACAGGCCAGCCAGTTGGTGGGGCCAGGCCAGGACCACACAGTCCCCAGAC
TCAGCTGGAAGTCTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
45 ATGGGGCACGGACTGTCCACCTTTTCTGATGTGTGTGTGTCAGCCTGTGCTGTGGCATAGACATGGATGCGAGGAC
CACTTTGGAGACTGGGGTGGCCTCAAGAGCACACAGAGAAGGGAAGAAGGGGCCATCACAGGATGCCAGCCCCCTG
CCTGGGTTGGGGCACTCAGCCACGACAGCCCCCTTCTGGGTATTTATTCTCTATTTATTGGGGATAGGAGAAG
AGGCATCTGCCTGGGTGGGACAGGCCCTTCAGCCCCCTTCTCNCCTCCCCGCTGGCCAGGGCAGGGCCACCCCA
CTCTACCTCCTTAGCTTTCCCTGTGCCACTTTGACTCAGAGGCTGGGAGCATAGCAGAGGGGCCAGGCCAGGCA
50 GAGCTGACGGGAGGCCCCAGCTCTGAGGGGAGGGGGTC

SEQ ID NO:431

>GL3_9.67_A_M13R Direction: anti-sense

CGGCAGCAAAACAGANCCTGCCTAACAGGACCCANCCAGTTGGTGGGGCCAGGCCAGGACCACACAGTCCCCAG
55 ACTCAGCTGGAAGTCTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGTCTACTC
GGATGGGGCACGGACTGTCCACCTTTTCTGATGTGTGTGTGTCAGCCTGTGCTGTGGCATAGACATGGATGCGAGG
ACCACTTTGGAGACTGGGGTGGCCTCAAGAGCACACAGAGAAGGGAAGAAGGGGCCATCACAGGATGCCAGCCCC
TGCCTGGGTTGGGGCACTCAGCCACGACAGCCCCCTTCTGGGTATTTATTCTCTATTTATTGGGGATAGGAGA
AGAGGCATCTGCCTGGGTGGGACAGGCCCTTCAGCCCCCTTCTCNCCTCCCCGACTGGCCAGGGCAGGGCCACCC
60 CACTCTACCTCCTNANATTCCCCTGTGC

SEQ ID NO:432

>GL3_9.67_B_M13F Direction: N/A

5 GCCAGTGTATTATTAGCAAGATGGAACCCAAAGGCGGCTGTGGCCTGGGCAGCAGAAGGCCACCAGGAGCCCCAC
CCATCTACCCAAGTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
10 GGGGAGCCTCTACCGGCCCCAGGCCTCTACCACGGACCCCCCTCCCCTCAGAGCTGGGGCCTCCCGTCAGCTCTGC
CTGGGCCTGGCCCCCTCTGCTATGCTCCCAGCCTCTGAGTCAAAGTGGCACAGGGAAAGCTAAGGAGGTAGAGTGG
GGTGGCCCTGCCCTGGCCAGGCGGGGAGGGGAGAAGGGGCTGAAGGGGCTGTCCCACCCAGGCAGGATGCCTCTT
CTCCTATCCCCAATAAATAGAGAATAAATACCCAGGAAGGGGCTGGTCTGAGTGGCCCCAAGGAGGAG
15 GGGCTGGCATCCTGTGATGGCCCCCTTCTTCCCTTCTCTGTGTGCTCTTGAGGCCACCCAGTCTCCAAAGTGGTC
CTCGCATCCATGTCTATGCCACAGCACAGGCTGACAACACACATCANAAAAGGTGGACAGTCCGTGCCCCATCCG
AGTAGGGCTTGCTCCCTCCCTTTGTCTGTAGATCTTGCGGANGCTGTCCAGCAGGTANACTTCCAGCTGANTC
TGGGGACTGTGTGGTCTGGCCTGGCCACCAACTGENTGGCCTGGTTAGGCAGGTCTGTTTTCTTGC

15 SEQ ID NO:433

>GL3_9.67_B_M13R Direction: anti-sense

CGGCAGAAAACAGAGCCTGCCTAACCAGGCCAGCCAGTTGGTGGGGCCAGGCCAGGACCACACAGTCCCAGAC
TCAGCTGGAAGTCTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
20 ATGGGGCAGGACTGTCCACCTTTTCTGATGTGTGTTGTCAGCCTGTGCTGTGGCATAGACATGGATGCGAGGAC
CACTTTGGAGACTGGGGTGGCCTCAAGAGCACACAGAGAAGGGGAAGAAGGGGCCATCACAGGATGCCAGCCCCTG
CCTGGGTTGGGGGCACTCAGCCACGACCAGCCCCCTTCTGGGTATTTATTTCTCTATTTATTGGGGATAGGAGAAG
AGGCATCCTGCCTGGGTGGGAGAGCCCCCTTCCAGCCCCCTTCCNCTCCCGCCTGGCCAGGGCAGGGCCACCCCA
CTCTACCTCCTTAGCTTTCCCTGTGCCACTTTGACTCAGAGGCTGGGAGCATAGCAGAGGGGCCAGGCCAGGCA
25 GAGCTGACGGGAGGCCCCAGCTCTGAGGGGAGGGGTCCGTGGTAGAGGCCTGGGGCCGGTAGAGGCTCCCCAGG
GCTCCCTTATGTCCACCACTTCAGGGGATGGGTGTG

SEQ ID NO:434

>GL3_9.67_C_M13F Direction: N/A

50 GCCAGTGTATTATTAGCAAGATGGAACCCAAAGGCGGCTGTGGCCTGGGCAGCAGAAGGCCACCAGGAGCCCCAC
CCATCTACCCAAGTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
GGGGAGCCTCTACCGGCCCCAGGCCTCTACCACGGACCCCCCTCCCCTCAGAGCTGGGGCCTCCCGTCAGCTCTGC
CTGGGCCTGGCCCCCTCTGCTATGCTCCCAGCCTCTGAGTCAAAGTGGCACAGGGAAAGCTAAGGAGGTAGAGTGG
GGTGGCCCTGCCCTGGCCAGGCGGGGAGGGGAGAAGGGGCTGAAGGGGCTGTCCCACCCAGGCAGGATGCCTCTT
35 CTCCTATCCCCAATAAATAGAGAATAAATACCCAGGAAGGGGCTGGTCTGAGTGGCCCCAAGGAGGAGGAG
GGGCTGGCATCCTGTGATGGCCCCCTTCTTCCCTTCTCTGTGTGCTCTTGAGGNCACCCAGTCTCCAAAGTGGTC
CTCGCATCCATGTCTATGCCACAGCACAGGCTGACAACACACATCANAAAAGGTGGACAGTCCGTGCCCCATCCG
ANTAGGGCTTGCTCCCTCCCTTTGTCTGTAAATC

SEQ ID NO:435

>GL3_9.67_D_M13R Direction: sense

50 GCCAGTGTATTATTAGCAAGATGGAACCCAAAGGCGGCTGTGGCCTGGGCAGCAGAAGGCCACCAGGAGCCCCAC
CCATCTACCCAAGTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
GGGGAGCCTCTACCGGCCCCAGGCCTCTACCACGGACCCCCCTCCCCTCAGAGCTGGGGCCTCCCGTCAGCTCTGC
45 CTGGGCCTGGCCCCCTCTGCTATGCTCCCAGCCTCTGAGTCAAAGTGGCACAGGGAAAGCTAANGAGGTAGAGTGG
GGTGGCCCTGCCCTGGCCAGGCGGGGAGGGGAGAAGGGGCTGAAGGGGCTGTCCCACCCAGGCAGGATGCCTCTT
CTCCTATCCCCAATAAATAGAGAATAAATACCCAGNAAGGGGCTGGTCTGAGTGGCCCCAAGGAGGAGGAG
GGGCTGGCATCCTGTGATGGCCCCCTTCTTCCCTTCTCTGTGTGCTCTTGAGGCCACCCAGTCTCCAAAGTGGTC
CTCGCATCCATGTCTATGCCACAGCACAGGCTGACAACACACATCANAAAAGGTGGACAG

50 SEQ ID NO:436

>GL3_9.67_PCR_G3F1 Direction: N/A

55 GCCAGTGTATTATTAGCAAGATGGAACCCAAAGGCGGCTGTGGCCTGGGCAGCAGAAGGCCACCAGGAGCCCCAC
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GGGGAGCCTCTACCGGCCCCAGGCCTCTACCACGGACCCCCCTCCCCTCAGAGCTGGGGCCTCCCGTCAGCTCTGC
CTGGGCCTGGCCCCCTCTGCTATGCTCCCAGCCTCTGAGTCAAAGTGGCACAGGGAAAGCTAAGGAGGTAGAGTGG
GGTGGCCCTGCCCTGGCCAGGCGGGGAGGGGAGAAGGGGCTGAAGGGGCTGTCCCACCCAGGCAGGATGCCTCTT
CTCCTATCCCCAATAAATAGAGAATAAATACCCAGGAAGGGGCTGGTCTGAGTGGCCCCAAGGAGGAGGAG
GGGCTGGCATCCTGTGATGGCCCCCTTCTTCCCTTCTCTGTGTGCTCTTGAGGCCACCCAGTCTCCAAAGTGGTC
CTCGCATCCATGTCTATGCCACAGCACAGGCTGACAACACACATCAGAAAAGGTGGACAGTCCGTGCCCCATCCG

AGTAGGGCTTGCTCCCTCCCTTTTGTCTGTAGATCTTGGCGGAGGCTGTCCAGCAGGTAGACTTCCAGCTGAGT
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SEQ ID NO:437

5 >gi|1061350|gb|U38276.1|HSU38276 Human semaphorin III family homolog mRNA,
complete cds
CTGACTGGTGCTCCCTCTCTTTTCATCTTGGGCTGTCTGCATGTGTCTCATTCCCCCACTCTCTCCTGTGC
CTCCCCCTCTACTCTAATAATCAGGTCCAGGTTTCTCTGTACTGGGAGAAGACCTGTGGCTGGAGCAGGCA
10 GGGATGCACCCATATCTGTTCCCATTCCTCCAGGTGGGAGGGAGAAGAGTAACCCACTTTATTGGCCAC
AGATGCAGGGGAGAAGGAGCATGTCTGGGAGCTGGAAAGAGCCCTAAGATCACCTGGTTTTCTAGAG
AGTGGAGCCTGCTTCTGCTAGGCCCTTCCCACAATGCTTGTGCGCGGTCTTCTTCTCTGGGCTTCCCT
ACTGACTGGGGCTGGCCATCCTTCCCTACCCAGGACCCTTCCCGGCCACGCCCGGTACGGCTCTCA
TTCAAAGAGCTGAAGGCCACAGGCACCGCCCACTTCTTCAACTTCTGTCTCAACACAACCGACTACCGAA
15 TCTTGCTCAAGGACGAGGACCACGACCGCATGTACGTGGGCAGCAAGGACTACGTGCTGTCCCTGGACCT
GCACGACATCAACCGCGAGCCCCCTCATTATACACTGGGCAGCCTCCCCACAGCGCATCGAGGAATGCGTG
CTCTCAGGCAAGGATGTCAACGGCGAGTGTGGGAACCTCGTCAGGCTCATCCAGCCCTGGAACCGAACAC
ACCTGTATGTGTGCGGGACAGGTGCCCTACAACCCCATGTGCACCTATGTGAACCGCGGACGCCGCGCCCA
GGATTACATCTTCTACCTGGAGCCTGAGCGACTCGAGTCAGGGAAGGGCAAGTGTCCGTACGATCCCCAAG
20 CTGGACACAGCATCGGCCCTCATCAATGAGGAGCTCTATGCTGGTGTGTACATCGATTTTATGGGCACTG
ATGCAGCCATCTTCCGCACACTTGGAAAGCAGACAGCATGCGCACGGATCAGTACAACCTCCCGGTGGCT
GAACGACCCGTCGTTTCATCCATGCTGAGCTCATTCCTGACAGTGCAGGAGAATGATGATAAGCTTTACTTC
TTCTTCCGTGAGCGGTGCGCAGAGGCGCCGAGAGCCCCGCGGTGTACGCCCGCATCGGGCGCATTTGGCC
TGAACGATGACGGTGGTCACTGTTGCCGTGGTCAACAAGTGGAGCACATTCTGAAGGCGCGGCTCGTCTG
25 CTCTGTCCCGGGCAGGATGGCATTTAGACTCACTTTGATGAGCTCCAGGACGTGTTTGTCCAGCAGACC
CAGGACGTGAGGAACCTGTCTATTACGCTGTCTTTACCTCCTCTGGCTCCGTGTTCCGAGGCTCTGCCG
TGTGTGTCTACTCCATGGCTGATATTGCGATGGTCTTCAACGGGCCCTTTGCCCCAAGAGGGGCCCAA
CTACAGTGGATGCCCTTCTCAGGGAAGATGCCCTACCCACGGCCGGGCACGTGCCCTGGTGGAACCTTC
ACGCCATCTATGAAGTCCACCAAGGATTATCTGTAGGTGATCAACTTCATGCGCAGCCACCCACTCA
TGTACCAGGCCGTGTACCTCTGCAGCGCGGCCCTTGGTAGTCCGCACAGGTGCTCCCTACCGCCTTAC
30 CACTATTGCGGTGGACACAGGTGGATTTCAGCCGACGGGCGCTATGAGGTGCTTTTCTGGGCACAGACCGC
GGGACAGTGCAGAAGGTCAATTGTGCTGCCCAAGGATGACCAGGAGATGGAGGAGCTCATGCTGGAGGAGG
TGGAGGTCTTCAAGGATCCAGCACCCGTCAAGACCATGACCATCTCTTCTAAGAGGCAACAACCTCTACGT
GGCGTCAGCCGTGGGTGTACACACCTGAGCCTGCACCGCTGCCAGGCGTATGGGGCTGCCTGTGCTGAC
TGCTGCCTTGCCCCGGGACCCCTTACTGTGCCCTGGGATGGCCAGGCCTGCTCCCGCTATACAGCATCCTCCA
35 AGAGCGGAGCCGCGCCGAGGACGTCCGGCACGGAAACCCCATCAGGCAGTGCCGTGGGTTCAACTCCAA
TGCCAACAAGAATGCCGTGGAGTCTGTGCAGTATGGCGTGGCCGGCAGCGCAGCCTTCCTTGAGTGCCAG
CCCCGCTCGCCCCAAGCCACTGTGTTAAGTGGCTGTTCCAGCGAGATCCTGGTGACCGGCGCCGAGAGATT
GTGCAGAGGACCGCTTCTGCGCACAGAGCAGGGCTTGTGCTCCGTGCACTGCAGCTCAGCGATCGTGG
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40 GGCCGGGACGCCGTCCATGCTGCCCTCTTCCCACCACTGTCCATGAGCGCCCCGCCACCCCCAGGCGCAG
GCCCCCAACGCCTCCTTACCAGGAGTTAGCCCAGCTGCTGGCCAGCCAGAAGTGGGCTCATCCACCA
GTACTGCCAGGGTTACTGGCGCCATGTGCCCCCAGCCCCAGGGAGGCTCCAGGGGCACCCCGGTCTCCT
GAGCCCCAGGACCAGAAAAAGCCCCGGAACCGCCGGCACCACCTCCGGACACATGAGGCCAGCTGCCTG
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45 ATATAAAAATATCTATATTCTATACACACCTGCCCCTGCAAAGACAGTATTTATTGGTGGGTTGAATAT
AGCCTGCCTCAGTGGCAGCATCCTCCAAAACCTTAGACCCATGCTGGTTCAGAGACGGCAGAAAACAGAGCC
TGCCTAACAGGCCAGCCAGTTAGTGGGGCCAGGCCAGGACACACAGTCCCAGACTCAGCTGGAGTCT
ACCTGCTGGACAGGCCTTGCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGGATGGGGC
ACGGACCGTCCACCTTTCTGATGTGTGTGTGTCAGCCTGTGCTGTGGCATAGACATGGATGCGAGGACCAC
50 TTTGGAGACTGGGGTGGCCTCAAGAGCACACAGAGAAGGGAAGAAGGGGCCATCACAGGATGCCACCCCT
GCCTTGGGTTGGGGGCACTCTGCCACGACCAGCCCCCTTCTTGGGTATTTATTCTCTATTTATTGGGGATA
GGAGAAGAGGCATCCTGCCTGGGTGGGACAGCCCCCTTGGGGCCCCCTTCTCCCCCTCCCCGCTGGCCAGGGA
GGGCCACCCACTCTACCTCCTTAGCTTTCCCTGTGCCACTTTGACTCAGAGGCTGGGAGCATAGCAGAG
GCCAGGCCAGGACAGAGCTGACGGGAGGCCACAGCTGAGGGGAGGGGTCCGTGGTAGAGCCTGGGGC
55 AGGTAGAGGCTCCCCAGGGCTCCCTTATGTCCACCACTTCAGGGGATGGGTGTGGATGTAATTAGCTCTG
GGGGCAGTTGGGTAGATGGGTGGGGGCTCCTGGTGGCTTCTGCTGCCAGGCCACAGCCGCTTTGGG
TTCCATCTTGCTAATAAACTAGGCTTTGGAACATAAAAAAAAAAAAAAAAAA

SEQ ID NO:438

60 >gi|1061351|gb|AAB18276.1| semaphorin III family homolog
MLVAGLLWASLLTGAWPSFPTQDHLPATPRVRLSFKELKATGTAHFFNLLNTTDYRILLKDEDHDMY

VGSKDYVLSLDLHDINREPLIIHWAASPQRIEECVLSGKDVNGECGNFVRLIQPWNRTHLVYVCGTGAYNP
 MCTYVNRGRRAQDYIFYLEPERLESKGKCPYDPKLDASALINEELYAGVYIDFMGTDAAIFRTLKGQT
 AMRTDQYNSRWLNDSFIAELIPDSAENDDKLYFFFRERSAEAPQSPAVYARIGRICLNDDGGHCCLVN
 5 KWSTFLKARLVCSVPGEDGIETHFDELQDVVFVQQTQDVNRNPVIYAVFTSSGSVFRGSAVCVYSMADIRMV
 FNGPFAHKEGPNYQWMPFSGKMPYPRPGTCTPGGTFTPSMKSTKDYDPDEVINFMRSHPMLYQAVYPLQRRP
 LVVRTGAPYRLTTIAVDQVDSADGRYEVLFLGTDRGTQVKVIVLPKDDQEMEELMLEEVEVFKDPAPVKT
 MTISSKRQQLYVASAVGVTHLSLHRCQAYGAACADCLARDPYCAWDGQACSRYTASSKRRSRRQDVRHG
 NPIRQCRGFNSNANKNAVESVQYGVAGSAAFLECCQPRSPQATVKWLFQRDPGDRRREIRAEDRFLRTEQG
 10 LLLRALQLSDRGLYSTATENNFKHVVTRVQLHVLGRDAVHAALFPPPLSMSAPPPGAGPPTPPYQELAQ
 LLAQPEVGLIHQYCYQGYWRHVPPSPREAPGAPRSPEPQDQKKPRNRHHPDPT

SEQ ID NO:439

SPARC

>gi|4507170|ref|NM_003118.1| Homo sapiens secreted protein, acidic,
 15 cysteine-rich (osteonectin) (SPARC), mRNA
 CGGGAGAGCGCGCTCTGCCTGCCGCTGCCTGCCACTGAGGGTTCCCAGCACCATGAGGGCCTGGA
 TCTTCTTTCTCCTTTGCCTGGCCGGGAGGGCCTTGGCAGCCCCCTCAGCAAGAAGCCCTGCCTGATGAGAC
 AGAGGTGGTGGAAGAACTGTGGCAGAGGTGACTGAGGTATCTGTGGGAGCTAATCCTGTCCAGGTGGAA
 GTAGGAGAATTTGATGATGGTGACAGGAAACCGAAGAGGAGGTGGTGGCGGAAAATCCCTGCCAGAACC
 20 ACCACTGCAACACGGCAAGGTGTGCGAGCTGGATGAGAACAACACCCCATGTGCGTGTGCCAGGACCC
 CACCAGCTGCCAGCCCCCATTGGCGAGTTTGAGAAGGTGTGACAGCAATGACAACAAGACCTTCGACTCT
 TCCTGCCACTTCTTTGCCACAAAGTGCACCCTGGAGGGCACCAAGAAGGGCCACAAGCTCCACCTGGACT
 ACATCGGGCCTTGCAATACATCCCCCCTTGCTGGACTCTGAGCTGACCGAATTCCTCCCTGCGCATGCG
 GGACTGGCTCAAGAACGTCCTGGTCACCCTGTATGAGAGGGATGAGGACAACAACCTTCTGACTGAGAAG
 25 CAGAAGCTGCGGGTGAAGAAGATCCATGAGAATGAGAAGCGCCTGGAGGCAGGAGACCACCCCGTGGAGC
 TGCTGGCCCCGGGACTTCGAGAAGAACTATAACATGTACATCTTCCCTGTACACTGGCAGTTTCGGCCAGCT
 GGACCAGCACCCATTGACGGGTACCTCTCCACACCGAGCTGGCTCCACTGCGTGCTCCCCCTCATCCCC
 ATGGAGCATTGCACCACCCGCTTTTTCGAGACCTGTGACCTGGACAATGACAAGTACATCGCCCTGGATG
 AGTGGGCGGGCTGCTTCGGCATCAAGCAGAAGGATATCGACAAGGATCTTGTGATCTAAATCCACTCCTT
 30 CCACAGTACCGGATTCTCTCTTTAACCTCCCTTCGTGTTTCCCCCAATGTTTAAATGTTTGGATGGT
 TTGTTGTTCTGCCTGGAGACAAGGTGCTAACATAGATTTAAGTGAATACATTAACGGTGCTAAAAATGAA
 AATTCTAACCAAGACATGACATTCTTAGCTGTAACTTAATTAAGGCCTTTTCCACACGCATTAATA
 GTCCCATTTTCTCTTGCCATTTGTAGCTTTGCCCATTTGTCTTATTGGCACATGGGTGGACACGGATCTG
 CTGGGCTCTGCCTTAAACACACATTGCAGCTTCAACTTTTCTCTTTAGTGTTCTGTTTGAACTAATACT
 35 TACCGAGTCAGACTTTGTGTTTCAATTTTCAAGGTCTTGGCTGCCTGTGGGCTTCCCCAGGTGGCCTG
 GAGGTGGGCAAGGGAAGTAAACAGACACACGATGTTGTCAAGGATGGTTTTGGGACTAGAGGCTCAGTGG
 TGGGAGAGATCCCTGCAGAATCCACCAACGAGAAGCTGTTTGCCTGAGGCTGTAAGTGAAGAAAGATT
 CTGGGGCTGTCTTATGAAAATATAGACATTCTCACAAGCCAGTTCATCACCATTTCCTCTTTTACCT
 TTCAGTGAGTTTCTTTTACATTAGGCTGTTGGTTCAAACCTTTTGGGAGCACGGACTGTCAGTTCTCTG
 40 GGAAGTGGTCAGCGCATCTGCAGGGCTTCTCCTCTGTCTTTTGGAGAACCAGGGCTCTTCTCAGGG
 GCTCTAGGGACTGCCAGGCTGTTTTCAGCCAGGAAGGCCAAAATCAAGAGTGAGATGTAGAAAGTTGTAAA
 ATAGAAAAAGTGGAGTTGGTGAATCGGTTGTTCTTTTCTCATTGAGATGATGTCATAAGGTTTGTAG
 CATGTTCTCTCTTTTCTTACCCTCCCCTTTGTTCTTCTATTAATCAAGAGAACTTCAAAGTTAATGGG
 45 ATGGTCCGATCTCACAGGCTGAGAACTCGTTACCTCCAAGCATTTTCATGAAAAAGCTGCTTCTTATTA
 TCATACAACTCTCACCATGATGTGAAGAGTTTCACAAATCTTTCAAATAAAAAAGTAATGACTTAGAAA
 CTGAAAAA

SEQ ID NO:440

>gi|4507171|ref|NP_003109.1| secreted protein, acidic, cysteine-rich
 50 (osteonectin); Osteonectin (secreted protein, acidic, cysteine-rich) [Homo
 sapiens]
 MRWIFFLLCLAGRALAAPQOEALPDETEVVEETVAEVTEVSVGANPVQVEVGEFDDGAEEETEEVVAEN
 PCQNHCKHKGKVCELDENTPMVCVCQDPTSCPAPIGEFEKVCSNDNKTDFDSSCHFATKCTLEGTGKKGHK
 LHLDDYIGPKYIPCLDSELTEFLMRDNLKLVLTLYERDEDNNLLTEKQKLRVKKIHENEKRLAEGD
 55 HPVELLARDFEKNYNMYIFPVHWQFGQLDQHPIDGYLSHTELAPLAPLIPMEHCTTRFFETCDLNDKY
 IALDEWAGCFGIKQKDKDLVI

SEQ ID NO:441

ssDNA binding protein-1

>GL1_4_1_G3F1 Direction: sense

CTGGCAGACCCTGGCCCAATCCTAACAGTGCTAACTCAATTCCATACTCCTCCTCATCACCTGGCTACCTATGTG
GGACCCCCTGGNTGGTGGCGGTCCCTCCAGGAACACCCATTATGCCAGTCCCGCAGATTCAACAAATTCAGTGA
CAACATCTACACAATGATTAATCCAGTGCCGCCTGGAGGCAGCCGGTCCAACCTCCCGATGGGTCCCGGCTCGAA
CGGTCCGATGGGCGGCATGGGTGGCATGGAGCCACACCACATGAATGGATCATTAGGGTCAGGCGACATAGACGG
NCTTCCAAAAAATTCCTCAACAACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAG

SEQ ID NO:442

>GL1_4_1_G3R1 Direction: anti-sense

CTCGCCGTCATCTCGAGGGGTGCCTGGAGGATTGCTAATGCCACTTATGTTGTTAGGAGAATTTTTTGGAAAGTCC
GTCTATGTCGCCTGACCCTAATGATCCATTTCATGTGGTGTGGCTCCATGCCACCCATGCCGCCCATCGGACCGTT
CGAGCCGGGACCCATCGGGAAGTTGGACCGGCTGCCTCCAGGCGGCACTGGATTAATCATTGTGTAGATGTTGTC
ACTGGAATTTGTTGAATCTGCGGGACTGGGCATAATGGGTGTTCTGGAGGACCGCCACCACCAGGGGGTCCAC
ATAGGTACCAGGTGATGAGGAGGAGTATGGAATTGAGTTAGCACTGTTAGGATTGGGCCAGGGTCTGCCAG

SEQ ID NO:443

>GL1_4_2_G3F1 Direction: sense

CTGGCAGACCCTGGCCCAATCCTAACAGTGCTAACTCAATTCCATACTCCTCCTCATCACCTGGTACCTATGTGG
GACCCCCTGGCTGGTGGCGGTCCCTCCAGGAACACCCATTATGCCAGTCCCGCAGATTCAACAAATTCAGTGAC
AACATCTACACAATGATTAATCCAGTGCCGCCTGGAGGCAGCCGGTCCAACCTCCCGATGGGTCCCGGCTCGAAC
GGTCCGATGGGCGGCATGGGTGGCATGGAGCCACACCACATGAATGGATCATTAGGGTCAGGCGACATAGACGGA
CTTCCAAAAAATTCCTCAACAACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAG

SEQ ID NO:444

>GL1_4_2_G3R1 Direction: anti-sense

CTCGNCGATCATCTCNAGGGGTGCCTGTAAGGATNGCATAAGTGCCACTTATGTTGTNAGGAGAATTTTTTGGAA
GTCCGTCTATGTCGCCTGACCCTAATGATCCATTTCATGTGGTGTGGCTCCATGCCACCCATGCCGCCCATCGGAC
CGTTCGAGCCGGGACCCATCGGGAAGTTGGACCGGCTGCCTCCAGGCGGCACTGGATTAATCATTGTGTAGATGT
TGTCATGGAATTTGTTGAATCTGCGGGACTGGGCATAATGGGTGTTCTGGAGGACCGCCACCACCAGGGGGTC
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SEQ ID NO:445

>gi|21314683|ref|NM_018070.2| Homo sapiens single stranded DNA binding
protein 3 (SSBP3), mRNA

CCGCGGCCGGGGCTGACGCTTTGACAGCTGGAAAGAGCGCGGAGCCAGCGCCTGGGGGGGAGGGAGGGGA
GCGCGCGGAGGAGAGCGCCAGCGAGCGAGAGCGAGCGCGCGGGGAGGGGGCCGGGAGCGAGGGGC
AGCTCGGGAGAGCCGAGCGGTAGCGGCGGGCGGCGGCGGCGAGGCTCGGCGCCCTCTTCCCTGC
AAACCATGTTTGCCAAAGGCAAAGGCTCGGCGGTGCCCTCGGATGGGCAGGCTCGGGAAGAGTTAGCTTT
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ATCCCGCCAGGTTTCTTTCAGGGTCTCCGGGGTACAGCCCTCGCCGCACGCACAGCCTCCACCTCACA
ATCCTAGCAGCATGATGGGACCCACAGTCAGCCTCCGGGAGGAGTTCTGGGACACAGCCATTGCTGCC
CAATTCCTATGGATCCACACGACAACAAGGCCACCCCAACATGGGAGGATCAATGCAGAGAATGAACCT
CCCCGAGGCATGGGGCCCATGGGTCCCGGCCACAGAATTACGGCAGCGGCATGAGACCACCACCCAAC
CCCTCGGCCCCGCCATGCCCGGGATTAACATGGGCCCGGGAGCTGGCAGACCCTGGCCCAATCCTAACAG
TGCTAACTCAATTCATACTCCTCCTCATCACCTGGTACCTATGTGGGACCCCTGGTGGTGGCGGTCTCT
CCAGGAACACCCATATGCCCAGTCCCGCAGATTCAACAAATTCAGTGACAACATCTACACAATGATTA
ATCCAGTGCCGCTGGAGGCAGCCGGTCCAACCTCCGATGGGTCCCGGCTCGGACGGTCCGATGGGCGG
CATGGGTGGCATGGAGCCACACCACATGAATGGATCATTAGGGTCAGGCGACATAGACGGACTTCAAAA
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GGAATTCCTCCACTCCTTTCAGAACGACAATTATCTCCAAGCATGACGATGAGTGTGTGATCCCCCT
TCTCCGAGACGCTGAGAGAGCAGGCATTGTCAGGCGGGAAGATGCCAGAAATTATGCAAGAAGTGAGGTGT
CATTATCCAGGAGCTGGTGGGGAGGGCATCTCCCTGCTCCCTCAACCCCTCCACCCCATCCACGCCC
CCTACCTTTCCCAATTTTAGTTTCATGCAATAAAAAGGCCAAAC'TTTTTATTCCATAAAACAAAAA
AAAAAAAAAAAAAAAAAAAA

SEQ ID NO:446

>gi|21314684|ref|NP_060540.2| single stranded DNA binding protein 3;
sequence-specific single-stranded-DNA-binding protein [Homo sapiens]
MFAKGKGSAPVSDGQAREKLALYVYELLHVGAQKSAQTFLSEIRWEKNITLGEPPGFLHSWWCVFWDLY
CAAPERDRTCEHSSEAKAFHDYSA AAPSPVLGNIPNDGMPGGPIPPGFFQGPFGSQPSPHAQPPPHNP
SSMMGPHSQPPGGVPGTQPLLPNSMDPTRQQGHPNMGGSMORMNPGRMGPMGPGPQNYGSGMRPPPNLS
GPAMPGINMGPAGRPWPNPNSANSIPYSSSSPGTYVGPFGGGGPPGTPIMPSPADSTNSSDNIYTMINP
VPPGGSRSNFPMGPGSDGPMGGMGMEPHMNGSLGSGDIDGLPKNSPNNISGISNPPGTPRDDGELGGN
FLHSFQNDNYSPTSMTSV

SEQ ID NO:447

SUMO-specific protease-1 (SUSP-1)

>G3_1_41_PCR_G3F1 Direction: sense

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GTATAGGCCCGTCTGAACGTGGGAGCGCAGCCCGCCTGACGGCTGAGCCCGAGGCCCGCAACCTGCGGCGTCTA
CCCTCCTCCGGCGCGGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAGAAGGAGGCGGCGT
GGGAGGAGGAAGATGGCGGCGCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAAGCTTTGGCTAGA
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SEQ ID NO:448

>GL3_1.41_A_M13F Direction: sense

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TGGCCTGCCTTTGTATAGGCCCGTCTGAACGTGGGAGCGCAGCCCGCCTGACGGCTGAGCCCGAGGCCCGCAACC
CTGCGGCGTCTACCTCCTCCGGCGCGGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAGA
AGGAGGCGGCGTGGGAGGAGGAAGATGGCGGCCCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAA
GCTTTGGCTAGATCAGAGTCTAAGAGAGATGGAGCCGCANAACCAGCACAGTGGTTAGATAGATAAAGCGGCCGC
TCGACTAGTCTGAGGTCTGATACTCACTGACTGTCTGAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTG
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AATTCACACAACA

SEQ ID NO:449

>GL3_1.41_A_M13R Direction: anti-sense

ATCACTAGTAACGGCCGCGCAGTGTGCTGGAATTCGCCCTTACGACAGTCAGTGAGTATCAGACCTCAGACTAGTC
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GCTTCCAGAAAAGTAATCTCCCTGCGCTACCGCCGCTCTTGCCGGCCGCGCATCTTCTCTCCACGCCGCTC
CTTCTTAATCCATGGCCACACCGCCGCGCTGCTCGCCGGGATGAGGGGCGCGCCGGAGGAGGGTAGACGCCGC
AGGGTTGCGGGCCTCGGGCTCAGCCGTGAGGCGGGCTGCGCTCCACGTTTACAGCGGCCCTATACAAAGGCAGGC
CAGGCGCGCCCGGGCCTGTCCGCGGGCTGGCGGGCAGCGAGGCCCGCGGCCCGAGCTTCTCAGGCCCTCTCCGGGG
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CC

SEQ ID NO:450

>GL3_1.41_B_M13F Direction: sense

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TGGCCTGCCTTTGTATAGGCCCGTCTGAACGTGGGAGCGCAGCCCGCCTGACGGCTGAGCCCGAGGCCCGCAACC
CTGCGGCGTCTACCTCCTCCGGCGCGGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAGA
AGGAGGCGGCGTGGGAGGAGGAAGATGGCGGCCCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAA
GCTTTGGCTAGATCAGAGTCTAAGAGAGATGGAGCCGCAGAACCAGCACAGTGGTTAGATAGATAAAGCGGCCGC
TCGACTAGTCTGAGGTCTGATACTCACTGACTGTCTGAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGG
ATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTTGTGAAATTGTTATCCGCTCACAA
TTCCACACAACATACGAGCCGGAAGCAT

SEQ ID NO:451

>GL3_1.41_B_M13R Direction: anti-sense

CGGATCACTAGTAACGGCCGCGCAGTGTGCTGGAATTCGCCCTTTCGACAGTCAGTGAGTATCAGACCTCAGACTAG
TCGAGCGGCCGCTTTATCTATCTAACCAGTGTGCTGGTTCTGCGGCTCCATCTCTCTTAGACTCTGATCTAGCCA
AAGCTTCCAGAAAAGTAATCTCCCTGCGCTACCGCCGCTCTTGCCGGCCGCGCATCTTCTCTCCACGCCGCC

TCCTTCTTAATCCATGGCCACACCGCCGCGTGTCTGCCGGGATGAGGGGCCGCGCCGGAGGAGGGTAGACGCC
GCAGGGTTGCGGGCCTCGGGCTCAGCCGTAGGCGGGCTGCGCTCCACGTTTCAGACGGGCCTATACAAAGGCAG
GCCAGGCGCGCCCGGGCCTGTCCGCGGGCTGGCGGGCAGCGAGGCCCGCGGCCGAGCTTCTCAGGCCCTCTCCGG
GGGAACGCGACCGGCGACGACGACGACGCGCTTCCCGGGCCCGGTTCTCTCGGCCACGACTCCCCATCCACC
5 GCCC

SEQ ID NO:452

>GL3_1.41_C_M13F Direction: sense

GGGCGGTGGATGGGGAGTCGTGGGCCGAGAGGAACCGGGCCCGGGAAGCGCCGTCTGTCGTCTGCCGGTCTGCGT
10 TCCCCCGGAGAGGCCTGAGAAGCTCGGGCCGCGGGCCTCGCTGCCCGCCAGCCCGCGGACAGGCCCGGGCGCGCC
TGGCCTGCCCTTTGTATAGGCCCGTCTGAACGTGGGAGCGCAGCCCGCCTGACGGCTGAGCCCGAGGCCCGCAACC
CTGCGGCGTCTACCCTCCTCCGGCGCGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAAGA
AGGAGGCGGCGTGGGAGGAGGAAGATGGCGGCCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAA
GCTTTGGCTAGATCAGAGTCTAAGAGAGATGGAGCCGCAGAACCAGCACAGTGGTTAGATAGATAAAGCGGCCGC
15 TCGACTAGTCTGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTG
GATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCC

SEQ ID NO:453

>GL3_1.41_C_M13R Direction: anti-sense

GCTCGGATCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTACGACAGTCAGTGAGTATCAGACCTCAGA
20 CTAGTCGAGCGGCCGCTTTATCTATCTAACCAGTGTGCTGTTCTGCGGCTCCATCTCTCTTAGACTCTGATCTA
GCCAAAGCTTCCAGAAAAGTAATCTCCCTGCGCTACCGCCGCTCTTGCCGGCCGCCATCTTCTCTCCACGC
CGCCTCCTTCTTAATCCATGGCCACACCGCCGCGTGTCTGCCGGGATGAGGGGCCGCGCCGAGGAGGGTAGA
CGCCGCAGGGTTGCGGGCCTCGGGCTCAGCCGTAGGCGGGCTGCGCTCCACGTTTCAGACGGGCCTATACAAAG
25 GCAGGCCAGGCGCGCCCGGGCCTGTCCGCGGGCTGGCGGGCAGCGAGGCCCGCGGCCGAGCTTCTCAGGCCCTCT
CCGGGGGAACGCGACCGGCGACGACGACGACGCGCTTCCCGGGCCCGGTTCTCTCGGCCACGACTCCCCATC
CACC GCC

SEQ ID NO:454

>GL3_1.41_D_M13F Direction: sense

GGGCGGTGGATGGGGAGTCGTGGGCCGAGAGGAACCGGGCCCGGGAAGCGCCGTCTGTCGTCTGCCGGTCTGCGT
30 TCCCCCGGAGAGGCCTGAGAAGCTCGGGCCGCGGGCCTCGCTGCCCGCCAGCCCGCGGACAGGCCCGGGCGCGCC
TGGCCTGCCCTTTGTATAGGCCCGTCTGAACGTGGGAGCGCAGCCCGCCTGACGGCTGAGCCCGAGGCCCGCAACC
CTGCGGCGTCTACCCTCCTCCGGCGCGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAAGA
35 AGGAGGCGGCGTGGGAGGAGGAAGATGGCGGCCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAA
GCTTTGGCTAGATCAGAGTCTAAGAGAGATGGAGCCGCAGAACCAGCACAGTGGTTAGATAGATAAAGCGGCCGC
TCGACTAGTCTGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTG
GATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCG

SEQ ID NO:455

>GL3_1.41_D_M13R Direction: anti-sense

GATCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTACGACAGTCAGTGAGTATCAGACCTCAGACTAGT
CGAGCGGCCGCTTTATCTATCTAACCAGTGTGCTGTTCTGCGGCTCCATCTCTCTTAGACTCTGATCTAGCCAA
45 AGCTTCCAGAAAAGTAATCTCCCTGCGCTACCGCCGCTCTTGCCGGCCGCCATCTTCTCTCCACGCCGCT
CCTTCTTAATCCATGGGCCACACCGCCGCCGTGCTCGCCGGGATGAGGGGCCGCGCCGGAGGAGGGTAGACGCCG
CAGGGTTGCGGGCCTCGGGCTCAGCCGTAGGCGGGCTGCGCTCCACGTTTCAGACGGGCCTATACAAAGGCAGG
CCAGGCGCGCCCGGGCCTGTCCGCGGGCTGGCGGGCAGCGAGGCCCGCGGCCGAGCTTCTCAGGCCTCTCCGGG
GGAACGCGACCGGCGACGACGACGACGCGCTTCCCGGGCCCGGTTCTCTCGGCCACGACTCCCCATCCACCG
50 CCC

SEQ ID NO:456

>gi|7662311|ref|NM_015571.1| Homo sapiens SUMO-1-specific protease (SUSP1), mRNA

ATGGCGGCCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAAGCTTTGGCTAGATCAGAGT
55 CTAAGAGAGATGGAGGTTTTAAAAATAATTGGAGCTTTGATCATGAAGAAGAAAGTGAAGGAGATACAGA
TAAAGATGGGACAAATCTGCTCAGTGTGGATGAAGATGAGGATTCTGAAACCTCAAAAGGAAAAAAGTTA
AATCGTCGATCTGAAATTGTTGCTAATAGCTCTGGTGAATTCATCTTGAAGACATATGTAAGACGAAACA
AGTCTGAAAGTTTTAAACTTTGAAAGGCAACCCAATTGGACTTAACATGTTGAGCAACAATAAGAAATT
GAGTGAATAATGCAAAATACGTCATTATGTTCTGGAAGTGTAGTTCATGGTAGACGTTTTCATCATGCT
60 CATGCACAGATACCAGTAGTAAAAACAGCAGCCCAAGCAGTCTGGACCGAAAAGAAAGGAAAGAATACC

CACCTCATGTCCAAAAAGTTGAAATTAATCCTGTAAGGTTAAGTCGGCTCCAAGGTGTTGAACGTATAAT
GAAGAAAACAGAAGAGTCCGAATCACAAGTGGAGCCTGAAATTAAGAGGAAAGTACAACAGAAAACGGCAC
TGTAAGTACCTATCAGCCTACTCCTCCTCTATCTCCTGCTTCAAAAAATGTTTAACCCATTTAGAGGATT
TGCAAAGAAATTTGCAGACAAGCTATTACTTTGAATGAGTCTACTGGACCATTATTAAGAAGCTCAATTCA
5 TCAGAAATTTCTGGAGGACAGAAGTCACAAAACACAGGATTAACAACCAAGAAGTTTTATGGCAACAATGTG
GAAAAGGTTCCAATTGATATTATTGTGAATTGTGATGACAGTAAACACACTTATTTACAGACTAATGGAA
AAGTCATTTTACCTGGGGCAAAAATACCCAAAATCACAACTTGAAAGAAAGGAAAACAAGTTTGTGACAG
CCTAAATGATCCAATCATTTTGTCCAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
10 ATATCTCCTCAGCCTGCTGATTCAGCATGTTCTTCCCCTGCACCATCCACTGGAAAAGTAGAAGCAGCAC
TAAATGAAAATACTTGCAGAGCAGAGCGTGAACCTACGAAGCATTCCAGAAGACTCAGAGTTAAATACAGT
TACATTGCCAAGAAAAGCAAGAATGAAAGACCAGTTTGGCAATTCTATTATCAACACACCTCTGAAACGT
CGTAAAGTGTTTTCTCAAGAACCCTCCAGATGCTTTAGCTTTAAGCTGCCAAAGTTCCTTTGACAGTGTCA
TTTTAAACTGTGCGAAGTATACGAGTAGGAACACTCTTCCGGCTGTTAATAGAGCCTGTAATTTTTTGT
15 AGATTTTATCAAGATACAGCTAGACGAACCAGACCATGATCCTGTAGAGATTATATTAAATACCTCTGAT
CTAACTAAATGTGAATGGTGTAAATGTCCGAAAATTACCTGTAGTGTCTTCAAGCAATTCAGCAGTTT
ATCAAAAGCTGAGCATCCAATGCAATGAATAAGGAGGATAAAGTTTGGAAATGATTGTAAAGGAGTAAA
TAAATTAACAAAATTTAGAAGAACAATATATAATTTTAAATTTTCAAAATGGCCTTGATCCTCCGGCAAAAT
ATGGTATTTGAAAGTATCATTAAATGAAATTTGGTATAAAGAATAACATCTCCAATTTTTTGGCAAAATTC
20 CCTTTGAAGAAGCTAATGGCAGACTTGTTCCTGTACAAAGAACCCTATGAAGAGAGCATCAAAGGAAGTGT
TGGGCAAAAGGAAAACAAAATTTAAACTGTATCATTTGAATCTAAAATACAACCTTAGAAGCAAAACAGTAA
TTTCAGTTTTTTTGATGAAGAAGAAGAACTGGAGAAAACACACCATCTTCATTGGCCCAGTAGAAAAGT
TGATAGTATATCCACCACCTCCAGCTAAGGGAGGCATCTCTGTTACCAATGAGGACCTGCAGTGTCTAAA
TGAAGGAGAAATTTTAAATGATGTTATTATAGACTTTTATTTGAAATACTTGGTGCTTGAAAACTGAAG
AAGGAAGACGCTGACCGAATTCATATATTCAGTTCTTTTTTCTATAAACGCCTTAATCAGAGAGAGAGGA
25 GAAATCATGAAACAACATACTGTCAATACAGCAAAAACGGCATGGGAGAGTAAAAACATGGACCCGGCA
CGTAGATATTTTTTGAGAAGGATTTTATTTTGTACCCCTTAATGAAGCTGCACACTGGTTTTTGGCTGTT
GTTTGTTCCTCCGGTTTGGAAAAACCAAGTATGAACCTAATCCTCATTACCATGAAAATGCTGTCTATAC
AGAAATGTTCAACTGTAGAGGACAGTTGTATTTCTTCTTCAGCCAGTGAAATGGAGAGTTGTTACAAAA
CTCTTCTGCCAAGCCTGTAATTAAGAAGATGCTAAACAAAAACATTGCATAGCTGTAATTGATTCCAAAT
30 CCTGGGCAGGAAGAAAGTGACCCCTCGTTATAAGAGAAACATATGCAGTGTAAAATACAGTGTGAAAAAA
TAAATCATACTGCGAGTGAAAATGAAGAATTCAATAAAGGAGAATCTACATCCAGAAAGTTGCTGATAG
GACTAAAAGTGAGAATGGCCTACAGAATGAAAGTTTAAAGTTCCACACATCATACAGATGGCTTAAGCAAA
ATCAGACTAAACTATAGCGATGAATCACCTGAAGCTGGTAAAATGCTTGAAGATGAACTCGTCGACTTCT
CAGAAGATCAGGATAACCAGGATGATAGCAGTGACGATGGATTCTCGCTGATGACAACCTGCAGTTTCTG
35 AATAGGACAGTGGCATTATAAGCCTACTATCTGTAAACAACCTTGTATCCTACTTATGGACTCACTCCGA
GGCCCTTCTCGGTCAAATGTTGTCAAATTTTGAAGAGTATTTAGAAGTGAATGGGAAGTTAAAAAAG
GAAGCAAAAGAAGTTTTCCAAAGATGTTATGAAGGGCTCTAATCCAAAAGTACCACAGCAAAAACACTT
CAGTGAAGTGTGGTGTATATGTATTGCAGTATGTAGAGAGCTTTTTTGAAGATCCAATTCTCAGTTTGA
CTACCTATGAATTTGGCAAACCTGGTTTCTCCACCAAGAATGAGAACAAAAAGAGAAGAAATCCGAAACA
40 TAATTTCTGAAGCTACAGGAAGATCAGAGCAAAAGAGAAAAGAAAGCATAAGGACACTTACTCAACAGAAGC
ACCTTTAGGCGAAGGAACAGAACAAATGTGTCAATAGTATCTCAGATTGACCATTTCTGTTACTTGTCTATT
TCTACTTTTCAGAACTAAATGACTTTCAAATTTGGGTATAGACAATAAAGAAGTGAAGTGCTCACTACTC
AGTGATTTGGAAATTTTGATGCTTGTATAAATGTGAGATAATTAATTTCCAAAGGCGTATGTATTAGTA
AAAGTCTGTAAATATGTTAATGAGGCCAATTTTCCAGCATTATATAATTATTTTTTCACTTGTAGGAA
45 GCTTTTGTATGTATTTTCTGTTAATAGTACCTTAAATTTGCAACTTCTAAACCCAAATAAAAAAGAAATA
TTTATAGGAGGAAATGATTAAATTTGATATTCTTTAGTGAACCTTGTTTAATTTCTCAGTGGGTGTGACATA
TTTCATGGGAATATTCAAATATCTATGGTAATATTTTACCCTTTATATTTGTTCTAAAATAAGTCAAAA
TGTGAAAAATAATATTAAATCTAAGATATTTTGAACCTAAGCATCTTTATATGCTTGTGTAAACAGGAACAAA
GTAACAGCCCTTCAATTCATATACCTGCTTGTGTTTCAAGTGAACCCAAAGAAATGTAATAAATATTTGTAAT
50 TTTACACAAAATATTTAAGAGGAAAGAGTATTAAGAGCAATTCAAAAAAGTAACCTTATACTACTAAAAA
AAAAATCTTGCATATATTATCATCAAATGCATTTTGAAGACATCAAAGACTCAGGTAAACTATTTT
GGTAAGTGACGCTTGAATTTCAAATATCCCGTGTACCTTTCTCTATTACAGCTTAAAGTATGCTACAAT
CTGTGTCATATAGTTAATTGATAAGCATTTTAAATCTGTGTAAACACAGGAATTTAAATAGGAATTTACT
ATTTTTTTAT

SEQ ID NO:457

>gi|7662312|ref|NP_056386.1| SUMO-1-specific protease [Homo sapiens]
MAAGKSGGSAGEITFLEALARSESKRDGGFKNNWSFDHEEESGDTDKDGTNLLSVDEDEDSETSKGKKL
NRRSEIVANSSGEFILKTYVRRNKSESFKTLKGNPIGLNMLSNNKKLSENMQNTSLCSGTVVHGRPFHHA
60 HAQIPVVKTAQSSLDKREKEYPPHVQKVEINPVRLSRLQGVERIMKKTEESQVEPEIKRKVQQRH
CSTYQPTPPLSPASKKCLTHLEDLQRNCRQAITLNESTGPLLRSTIHQNSGGQKSQNTGLTTKKFYGNV

EKVPIDIIVNCDDSKHTYLQTNKGKVLPGAKIPKITNLKERKTSLSLDLNDPIILSSDDDDDDNDRTNRRES
ISPQPADSACSSPAPSTGKVEAALNENTCRAERELRSIPEDSELNTVTLPRKARMKDQFGNSIINTPLKR
RKVFSQEPDALALSCQSSFDVILNCRSIRVGTFLRLLIEPVIFCLDFIKIQLDEPDHDPVEIILNTSD
LTKCEWCNVRKLPVVFLQAI PAVYQKLSIQLOMNKEDKVWNDCKGVNKLTLNLEEYIILIFQNGLDPPAN
5 MVFESIINEIGIKNNISNFFAKIPFEEANGRLVACTRTYEESIKGSCGQKENKIKTVSFESKIQLRSKQE
FQFFDEEEETGENHTIFIGPVEKLIVYPPPPAKGGISVTNEDLHCLNEGEFLNDVIIDFYLYLVLEKLEK
KEDADRIHIFSSFFYKRLNQRRERNHETTNLSIQQRHGRVKTWTRHVDIFEKDFIFVPLNEAAHWFLAV
VCFPGLEKPKYEPNPHYHENAVIQKSTVEDSCISSASEMESCSQNSSAKPVIKMLNKKHCIAVIDSN
PGQESDPRYKRNICSVKYSVKINHTASENEEFNKGESTSQKVADRTKSENGLQNESLSSTHTDGLSK
10 IRLNYSDESPEAGKMLEDELVDSEDOQDDSSDDGFLADDNCSSEIGQWHLKPTICKQPCILLMDSLR
GPSRSNVVKILREYLEVEWEVKKGSKRSFSKDVMMKGSNPKVPQQNNFSDCGVYVLQYVESFFENPILSFE
LPMNLANWFPPPRMRTKREIRNIILKLQEDQSKEKRKHKDTYSTEAPLGEGTEQCVNSISD

SEQ ID NO:458

Synaptophysin homologue (pantophysin)

>GL2_71_G03_G3F1 Direction: sense

ACAGGAACACAAAGACTGCAAAGGTAACATAGAATTGTGTCAGAAGAAGAGTAATCGCCTATGAGGACGTAATCTT
TCCAATTTACATCACATATGTTTACACCTGGAGGTGGCTGAAATGATGCCTCATTC AACCTGAATGGATAACCAA
AAGTAGCTGTAACAGTTTTATTCTCAGTAAGTGCAGGAGGACAATTCACCTGAATTTCTGTTTGGCCCTTAAAC
20 CTCCACAGGTGGCAAAGCAAAGATAGAAGCAATCCACTCGAGGACCTTGATGAAGCCGAGTGGCTCCTTGAGCG
GGTTGAGGTTGATCTGGAAGCCGCCGAGGACCCAGCGCAGTGGTTAGATAGATAAAGCGACCGCTCGACTAGTC
TGAGGTCTGATACTCACTGACTGTGCGTAAGGGCGAATTCGTTTAAACCTGCAGGACTAGTCCCTTTAGTGAGGGT
TAATCTGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAATTCACACA
ACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTTGCGTTG
25 CGCTCACTGGCCGCTTTCCAGTCGGGAAAACCTTGTCGTTGCCAGTGCATTAATGAATCGGCCAACGCCGCGGGG
NAGAGGNCGGGGTAGCGTNAATAGGGGGCGGCCCTTACCCGGTTTCTCCCGCTCANTTGAATCCGCTTGGCCC
CGGGCG

SEQ ID NO:459

>GL2_71_G04_G3F1 Direction: sense

ACAGGAACACAAAGACTGCAAAGGTAACATAGAATTGTGTCAGAAGAAGAGTAATCGCCTATGAGGACGTAATCTT
TCCAATTTACATCACATATGTTTACACCTGGAGGTGGCTGAAATGATGCCTCATTC AACCTGAATGGATAACCAA
AAGTAGCTGTAACAGTTTTATTCTCAGTAAGTGCAGGAGGACAATTCACCTGAATTTCTGTTTGGCCCTTAAAC
35 CTCCACAGGTGGCAAAGCAAAGATAGAAGCAATCCACTCGAGGACCTTGATGAAGCCGAGTGGCTCCTTGAGCG
GGTTGAGGTTGATCTGGAAGCCGCCGAGGACCCAGCGCAGTGGTTAGATAGATAAAGCGACCGCTCGACTAGTC
TGAGGTCTGATACTCACTGACTGTGCGTAAGGGCGAATTCGTTTAAACCTGCAGGACTAGTCCCTTTANTGAGGGT
TAATCTGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAATTCACACA
ACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTTGAGCTAACTCACATTAATTTGCG
40 TTTGCGCTCACTTGGGCCGCTTTCCAGGTTTCGGGGAAAACCTGTGTCGCCAGTTGCTTAATGAATCGGGCAACG
CGCGGGGAGAGGCGGTGGGTATNG

SEQ ID NO:460

>GL2_71_G05_G3F1 Direction: sense

ACAGGAACACAAAGACTGCAAAGGTAACATAGAATTGTGTCAGAAGAAGAGTAATCGCCTATGAGGACGTAATCTT
45 TCCAATTTACATCACATATGTTTACACCTGGAGGTGGCTGAAATGATGCCTCATTC AACCTGAATGGATAACCAA
AAGTAGCTGTAACAGTTTTATTCTCAGTAAGTGCAGGAGGACAATTCACCTGAATTTCTGTTTGGCCCTTAAAC
CTCCACAGGTGGCAAAGCAAAGATAGAAGCAATCCACTCGAGGACCTTGATGAAGCCGAGTGGCTCCTTGAGCG
GGTTGAGGTTGATCTGGAAGCCGCCGAGGACCCAGCACAGTGGTTAGATAGATAAAGCGGCCGCTCGACTAGTC
TGAGGTCTGATACTCACTGACTGTGCGTAAGGGCGAATTCGCGGCCGCTAAATTC AATTCGCCCTATAGTG

SEQ ID NO:461

>GL2_71_G06_G3F1 Direction: sense

ACAGGAACACAAAGACTGCAAAGGTAACATAGAATTGTGTCAGAAGAAGAGTAATCGCCTATGAGGACGTAATCTT
55 TCCAATTTACATCACATATGTTTACACCTGGAGGTGGCTGAAATGATGCCTCATTC AACCTGAATGGATAACCAA
AAGTAGCTGTAACAGTTTTATTCTCAGTAAGTGCAGGAGGACAATTCACCTGAATTTCTGTTTGGCCCTTAAAC
CTCCACAGGTGGCAAAGCAAAGATAGAAGCAATCCACTCGAGGACCTTGATGAAGCCGAGTGGCTCCTTGAGCG
GGTTGAGGTTGATCTGGAAGCCGCCGAGGACCCAGCACAGTGGTTAGATAGATAAAGCGGCCGCTCGACTAGTC
TGAGGTCTGATACTCACTGACTGTGCGTAAGGGCGAATTCGCGGCCGCTAAATTC AATTCGCCCTATAGTGAGTGC
TATTACAATTCAGTGGCCGTCGTTTACAACGTCGTGACTGGGAAAACCTTGGCGTTACCCCACTTAATCGCCTT
60 GCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGACCGATCGCCCTTCCCAACAGTTGCGCA

GCCTATACGTACGGCAGTTTAAAGGTTTACNACCTATTAAAGAGAGAGCCCGGTATCGTCTGTTGTGGATGTNC
AGAGTGATATTTATTTGGAACCCCGGGGAAAGAAT

SEQ ID NO:462

5 >gi|5803184|ref|NM_006754.1| Homo sapiens synaptophysin-like protein
(SYPL), mRNA
TGAACCGAGGCAAGGGGGCGCGGCACGCAGTATGGCGCCCAACATCTACTTGGTTCGCCAGCGGATCA
GTCGACTCGGCCAGAGGATGTCCGGCTTCCAGATCAACCTCAACCCGCTCAAGGAGCCACTCGGCTTCAT
CAAGGTCCTCGAGTGGATTGCTTCTATCTTTGCTTTTGCCACCTGTGGAGGTTTAAAGGGCCAAACAGAA
10 ATTCAAGTGAATTGTCTCTGCAGTTACTGAGAATAAACTGTTACAGCTACTTTTGGTTATCCATTCA
GGTTGAATGAGGCATCATTTTCAGCCACCTCCAGGTGTAAACATATGTGATGTAAATTGGAAAGATTACGT
CCTCATAGGCGATTACTCTTCTCTGCACAATTCTATGTTACCTTTGCAGTCTTTGTGTTCTCTGTACTGC
ATTGCTGCCCTTCTGCTTTATGTTGGCTACACGAGTCTGTATCTGGATAGTCGTAAACTTCCTATGATAG
ACTTTGTTGTTACACTTGTGTCCTTTTGTGGTTGGTGAGCAC TTCAGCCTGGGCTAAAGCTCTGAC
15 AGATATTAAATAGCTACTGGTCACAATATTATTGATGAACCTTCCGCCTTGTAAGAAGAAAGCAGTACTG
TGTTACTTTGGCTCTGTGACCAGTATGGGATCCCTAAATGTATCTGTGATATTTGGCTTTCTAAATATGA
TACTCTGGGGAGGAAATGCTTGGTTTGTGTACAAGGAGACCAGCCTACACAGTCCATCAAATACATCTGC
CCCTCATAGCCAAGGAGGTATTCCACCTCCTACCGGAATATAATTAAAGGGAGAAATACACTGTATGAAG
TATATGTTGATACATGATGACATGTTGCCAACACCTTGAGAAGCATTATTTGTTTCTAATAAAAGTAATGGC
20 TTTGTCAATATATGTTGGGTTTAAACCTTTGCTGCTTTTACATAAAGCCTGTGCCTTTCTAGAAAG
TTAAGATGTAAATGTATTCTCACATGTAAATTGAAAGTTCAGGGGTCTATTATGAAATGGATTACACAT
TTTAAATGAACCCATAATTTTCTCACTAAAGCTGTTTGCCCTCCAAAGTGTTTACACCTAAGCCTAACA
TGTATCGCTCATTCAGAAAACCTGTTATATTGTCATACCATAGTAGGAAGAAAACCTTTATTTGGAATAT
ACACTACTGTAAGTTTGTACAGATCATATACCTACCACCTGTCTTTGCTTAAAGAGCCTTGATTACATAA
25 ATATGTAGAAAAAACATATTGAGTTCAAATTTATATCTAACATTGTTTATGTTATGATTTTTTTTAAAT
TGCAAAGACTAGGTGTATATTTTCTGTTTTCTAAATGACCCGTGGTACTTAATAGGTGTACTAAAA
TTGTGTTGGGAGCAGGGATTGGAAATTTCTGAGAGATGTGTAGTTAATTAGTAATTCTGTTTCATGAGA
TATGATCTGTTATGCTAGTGGTTTAAATAGGCTTGCTATGTAAGTAGAACGTGGCTCAACTAGATATCTTA
TATGTATGGGCATTACCTCTTAGTGATATTTGTTTCTGCTCTTTGTTGCTCATGCTGTTTAAAGTGCAGG
30 CTGAGACCCAGCCTCTTTGTAAGTACAGTAAATAATCCACCGTTTTTACAGACCTAGTCAAAGGGTT
AAAAAATTAAGATTGCTTTCCATGTTTGAAATTTACCATTGAGAGTCAATGAAGTTGCTATTTTGAGTT
TAGCATTGATATTGTGAAAATAAGTGCAATTTGGATTTTCATGTTTCTTAATATTCATTCTTGTTTCACAA
ATGAATGATTAAGGAATTATGCATCATAAAGGAACCTAAGTGAGGTATATGATGAGTGTATTGCTTTTGC
ACACACATATAGGTATATTCTGAATACAAGCTTATTCATTTTGCTTCTTAATCTTTTTGTTGTACAGGGA
35 TTCAGGTTTCTTATTCTTACAACATGATTGTTTATATGTGAAGCACATCTTGCTGTTGCCTTATTTTGA
TGCTTTTATTCATGACAAGAATTGTCAATATAAGAATGTATATCTTTGCCGCAACCAATTTAATAAAGGA
GTTGAAAGAAAAA

SEQ ID NO:463

40 >gi|5803185|ref|NP_006745.1| synaptophysin-like protein; pantophysin [Homo
sapiens]
MAPNIYLVRQIRISRLGQRMISGFQINLNPLKEPLGFIKVLWIASIFAFATCGGFKGQTEIQVNCPPAVTE
NKTVTATFGYPFRLNEASFQPPPGVNICDVNWKDYVLIGDYSSSAQFYVTFVAVFVFLYCIALLLYVGYT
SLYLDNRKLPIDFVVTLVATFLWLVTSAWAKALTDIKIATGHNIIDELPPCKKAVLCYFGSVTSMGS
45 LNVSVIFGFLNMILWGGNAWFVYKETSLSHSPNTSAPHSQGGIPPTGI

SEQ ID NO:464

Thrombospondin-1

>GL2_199_2_M13R Direction: anti-sense

50 CCAATGTAGTTAGTGCAGGATGGCAGGGCTGGAACCATTCACCACGTTGTTGTCAAGGGTGAGGAGGACACTGGTA
GAGCTGGAGCAGCCTTTGTTCTCTGAGGATGTCTTCTGGTGTGGTTCCAAAGACAAACCTCACATTCTGCAGCACC
CCCTGGAAAATGTCA

SEQ ID NO:465

>GL2_199_1_M13R Direction: sense

55 TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACA
AAGGCTGCTCCAGCTCTACCAGTGTNCTCCTCACCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGGCATCC
GNACTAACTACATTGG

SEQ ID NO:466

>GL2_199_3_M13F Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAA
AGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:467

>GL2_66_F01_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCTGGCATCCGACTA
ACTACATTGG

SEQ ID NO:468

>GL2_66_F02_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
ACTAACTACATTGG

SEQ ID NO:469

>GL2_66_F03_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:470

>GL2_66_F04_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAA
AGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:471

>GL2_86_2A01_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
ACTAACTACATTGG

SEQ ID NO:472

>GL2_86_2A02_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:473

>GL2_86_2A03_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:474

>GL2_86_2A04_G3F1 Direction: N/A

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACAGCGTCTCCTCA

SEQ ID NO:475

>GL2_86_2A06_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAATCACACCAGAAGACATCCTCAGGAACAAAGG
CTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCGCAC
TAACTACATTGG

SEQ ID NO:476

>GL2_86_2A07_G3F1 Direction: sense

CGACATTTTCCAGGGGGTGCTGCAGAAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACAA
AGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:477

>GL2_86_2A08_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
ACTAACTACATTGG

SEQ ID NO:478

>GL2_86_2A09_G3F1 Direction: sense

GTGACATTATCCAGTGGGTGCTGCAGAAATGTGAGGTTTGTCTTTGGAACACACNCAGAAGACATCCTCAGGAAC
AAAGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGACAACAACGATGGTGAATGGTTCCAGCCCTGNCAT
CCGCACTAACTACATTGG

SEQ ID NO:479

>GL2_199_3_M13R Direction: anti-sense

CCAATGTAGTTAGTGCGGATGGCAGGGCTGGAACCATTCACCACGTTGTTGTCAAGGGTGAGGAGGACACTGGTA
GAGCTGGAGCAGCCTTTGTTCTTGAGGATGTCTTCTGGTGTGGTTCCAAAGACAAACCTCACATTCTGCAGCACC
CCCTGGAAATGTCA

SEQ ID NO:480

>GL2_86_2A05_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAAATGTGAGGTTTGTCTTTGGAACACACCAGAAGACATCCTCAGGAACAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
ACTAACTACATTGG

SEQ ID NO:481

>gi|4507484|ref|NM_003246.1| Homo sapiens thrombospondin 1 (THBS1), mRNA

GGACGCACAGGCATTCCCCGCGCCCCCTCCAGCCCTCGCCGCCCTCGCCACCGCTCCCGGCCGCGCGCTC
CGGTACACACAGGATCCCTGCTGGGCACCAACAGCTCCACCATGGGGCTGGCCTGGGGACTAGGCGTCCT
GTTCTGTATGCATGTGTGTCACCAACCGCATTCAGAGTCTGGCGGAGACAACAGCGTGTTTGACATC
TTTGAATCCACCGGGGCCCGCCGCAAGGGGTCTGGCGCCGAGTGGTGAAGGGCCCCGACCCTTCAGCC
CAGCTTTCCGCATCGAGGATGCCAACCTGATCCCCCTGTGCTGATGACAAGTTCCAAGACCTGGTGGA
TGCTGTGCGGGCAGAAAAAGGTTTCTCCTTCTGGCATCCCTGAGGCAGATGAAGAAGACCCGGGGCAG
CTGCTGGCCCTGGAGCGGAAAGACCACTCTGGCCAGGTCTTCAGCGTGGTGTCCAATGGCAAGGCGGGCA
CCCTGGACCTCAGCCTGACCGTCCAAGGAAAGCAGCACGTGGTGTCTGTGGAAGAAGCTCTCCTGGCAAC
CGGCCAGTGAAGAGCATCACCTGTTTGTGCAGGAAGACAGGGCCCAGCTGTACATCGACTGTGAAAAG
ATGGAGAATGCTGAGTTGGACGTCCCCATCCAAAGCGTCTTCACCAGAGACCTGGCCAGCATCGCCAGAC
TCCGCATCGCAAAGGGGGGCGTCAATGACAATTTCCAGGGGGTGCTGCAGAAATGTGAGGTTTGTCTTTGG
AACCACACCAGAAGACATCCTCAGGAACAAAGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGAC
AACAACGTGGTGAATGGTTCCAGCCCTGCCATCCGCACTAACTACATTGGCCACAAGACAAAGGACTTGC
AAGCCATCTGCGGCATCTCCTGTGATGAGCTGTCCAGCATGGTCTGGAACCTCAGGGGCCCTGCGCACCAT
TGTGACCACGCTGCAGGACAGCATCCGCAAAGTGACTGAAGAGAACAAGAGTTGGCCAATGAGCTGAGG
CGGCCTCCCCATATGCTATCACAACGGAGTTTCAGTACAGAAATAACGAGGAATGGACTGTTGATAGCTGCA
CTGAGTGTCACTGTGAGAACTCAGTTACCATCTGCAAAAAGGTGTCTGCCCCATCATGCCCTGCTCCAA
TGCCACAGTTCTTGATGGAGAATGCTGTCTCGCTGTGGCCAGCGACTCTGCGGACGATGGCTGGTCT
CCATGGTCCGAGTGGACCTCCTGTTCTACGAGCTGTGGCAATGGAATTCAGCAGCGCGGCCGCTCCTGCG
ATAGCCTCAACAACCGATGTGAGGGCTCCTCGGTCCAGACACGGACCTGCCACATTTCAGGAGTGTGACAA
AAGATTTAAACAGGATGGTGGCTGGAGCCACTGGTCCCCGTGGTTCATCTTGTCTGTGACATGTGGTGTAT
GGTGTGATCACAAAGGATCCGGCTCTGCAACTCTCCAGCCCCCAGATGAATGGGAAACCCGTGAAGGCG
AAGCGCGGGAGACCAAAGCCTGCAAGAAAGACGCTGCCCATCAATGGAGGCTGGGGTCTCTTGGTCACC
ATGGGACATCTGTTCTGTACCTGTGGAGGAGGGGTACAGAAAACGTAGTCGTCTCTGCAACAACCCCGCA
CCCCAGTTTGGAGGCAAGGACTGCGTTGGTGTATGTAACAGAAAACAGATCTGCAACAAGCAGGACTGTC
CAATTGATGGATGCCTGTCCAATCCCTGCTTTGCCGGCGTGAAGTGTAAGTACTAGCTACCCTGATGGCAGCTG
GAAATGTGGTGTCTTGTCCCCCTGGTTACAGTGGAAATGGCATCCAGTGCACAGATGTTGATGAGTGCAA
GAAGTGCCTGATGCCTGCTTCAACCACAATGGAGAGCACCGGTGTGAGAACACGGACCCCGGCTACAAC

SEQ ID NO:482
>gi|4507485|ref|NP_003237.1| thrombospondin 1 [Homo sapiens]
MGLAWGLGVFLMHVCGTNRIPESGGDNSVFDIFELTGAARKGSGRRLVKGPDPSSPAFRIEDANLIPPV
PDDKFQDLVDRAEKGFLLLASLRQMKKTRGTLLALERKDHSGQVFSVVSNGKAGTLDLSLTVQGQKHV
VSVEEALLATGQWKSTLTFVQEDRAQLYIDCEKMENAELDVPIQSVFTRDLASIARLRIAKGGVNDNFQG
VLQNVRFVFGTTPEDILRNKGCSSTSVLLTLNNVVNGSSPAIRTNYIGHKTKDLQAICGISCELSSM

VLELRGLRTIVTTLQDSIRKVTEENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKK
VSCPIMPSCSNATVPDGECCPRCWPSDSADDGWSWPSEWTSCSTSCGNGIQQRGRSCDSLNNRCEGSSVQT
RTCHIQECDKRFKQDGGWSHWSWSSCSVTGCGDVITRIRLCNSPSPQMNGKPCGEARETKACKKDACP
INGGWGPWSPWDICSVTCGGGVQKRSRLCNPAPQFGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGV
5 KCTSYPDGSKWCKGACPPGYSNGIQCTDVDECKEVPDACFNHNGEHRCENTDPGYNCLPCPPRFTGSQPF
GQGVHEHATANKQVCKPRNPCTDGTDCNKNACNYLGHYSDFMYRCECKPGYAGNGIICGEDTDLGDWPN
ENLVCVANATYHCKKDNCPNLPSNGQEDYDKDGI G DACDDDDNDKI PDDRDNCPFHYNPAQYDYDRDDV
GDRCDNCPYHNHPDQADTDNNGEGDACAADIDGGILNERDNCQYVYNVDQRDTMDMGVGDQCDNCPLEH
10 NPDQLDSDSDRIGDTCNNDQDIDEDGHQNNLDNCPYVNPANQADHDKDGKGDACDHDDNDGIPDDKDN
RLVFPNDQKDSGDGRGDACKDDFDHDSVPDIDDICPENVDISETDFRRFQMIPLDPKGTSONDPNVVVR
HQGKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDDYAGFVFGYQSSSRFYVVMWKQVTQSYWDT
NPTRAQGYSLSVKVVNSTTGPGEHLRNALWHTGNTPGQVRTLWHDPRHIGWKDFTAYRWRLSHRPKTGF
IRVVMYEGKKIMADSGPIYDKTYAGGRLGLFVFSQEMVFFSDLKYECRDP

SEQ ID NO:483

Transgelin 2

>GL3_30H_PCR_G3F1 Direction: sense

CACTGTACCCGAGGGGAGGCCCCAGTAAAGAAGATCAGGCCTCCACCATGGCCTTCAAGCAGATGGAGCAGATC
TCTCAGTTCCTG

SEQ ID NO:484

>gi|4507356|ref|NM_003564.1| Homo sapiens transgelin 2 (TAGLN2), mRNA
GCCCTTGCCCTTGAGTCAGTGCCTGCTCTCCAGCCCGCTTGAACGCTCCCCGCAGCCACCGCCACCCATT
GGAATGGCCAACAGGGGACCTGCATATGGCCTGAGCCGGGAGGTGCAGCAGAAGATTGAGAAACAATATG
25 ATGCAGATCTGGAGCAGATCCTGATCCAGTGGATCACCACCCAGTGCCGAAAGGATGTGGGCCGGCCCCA
GCCTGGACGCGAGAAGTTCAGAACTGGCTCAAGGATGGCAGCGTGCTATGTGAGCTCATTAATGCACTG
TACCCCGAGGGGAGGCCCCAGTAAAGAAGATCCAGGCCTCCACCATGGCCTTCAAGCAGATGGAGCAGA
TCTCTCAGTTCCTGCAAGCAGCTGAGCGCTATGGCATTAAACACCACTGACATCTTCCAAACTGTGGACCT
30 CTGGGAAGGAAAGAACATGGCCTGTGTGACGCGGACGTGATGAATCTGGGTGGGCTGGCAGTAGCCCGA
GATGATGGGCTCTTCTCTGGGGATCCCAACTGGTTCCCTAAGAAATCCAAGGAGAATCCTCGGAACCTCT
CAGATAACCACTGCAAGAGGGCAAGAAGCTGATCGGGTTACAGATGGGCACCAACCGCGGGCGTCTCA
GGCAGGCATGACTGGCTACGGGATGCCACGCCAGATCCTCTGATCCCACCCAGGCCTTGCCCTGCCCT
CCCACGAATGGTTAAT
35 TCCCCATGCTTACTAATAACATTCCTTCCCCATAGCCATCAAACTGGACCAACTGGCCTCTTCTCTTTC
CCCTGGGACCAAAATTTAGGGGCTCAGTCCCTCACCGCCATGCCCTGGCCTATTCTGTCTCTCTCTCTT
CCCCCTGGCCTGTTCTGTCTCTGAGCTCTGTCTCTCCGTTTCCATTCATGGCTGGGAGTCACTGATGCTG
CCTCTGCCTTCTGATGCTGGACTGGCCTTGCTTCTACAAGTATGCTTCTCCACAGCTGTGGCTGCAGGA
40 ACTTAATTTATAGGGAGGAGCCTGTGGCAGCTGCTGCCCCAGCCACAGCTGCACTGACTGTGCTCACCAC
ACATCTGGGGCAGCCTTCCCTGGCAGGGGCCCTCGTGGCTTCTCATTTTCCATTCCCTTCACTGTGGCTA
AGGGGTGGGGTGAGGGGATGGAGAGGGAGGGCTGCCTACCATGGTCTGGGGCTTGAGGAAGATGAGTTTG
TTGATTTAAATAAGAATTTGTCAATTTTG

SEQ ID NO:485

>gi|4507357|ref|NP_003555.1| transgelin 2; SM22-alpha homolog [Homo sapiens]

MANRGPAYGLSREVQKIEKQYDADLEQILIQWITTQCRKDVGRPQPGRENFNWLKDGTVLCELINALY
PEGQAPVKKIQASTMAFKQMEQISQFLQAERYGINTTDIFQTVDLWEGKNMACVQRTLMMNLGGLAVARD
50 DGLFSGDPNWFPPKSKENPRNFSNQLQEGKNVIGLQMGNTNRGASQAGMTGYGMPRQIL

SEQ ID NO:486

Vigilin

>GL3_43A1_1_M13F Direction: anti-sense

CCGGGCAGCTTCGCAGTTGGCTCGCTTGCTGTGATGATAATGGTCTCTGAATTGCTATTCTCTGCTGGAAGGGT
CGATTTTGGTGTGTGCTTTCTTACGAATCTTTTAAATGTTGCGCTCCTTTCCCAATGATATTCTTGTGAAACT
55 GTTGAAGATCGGAACAGAAATTGAATAGCTATTTTCCACCAGATCTGCCACCATCTTCTGCATGTATTTTGTGC
ATTTTTCACCTCATCTTAGGTCTCTGAGCTGGACAATGTCACTTTTTTGTGCTGGG

SEQ ID NO:487

>GL3_43A1_1_M13R Direction: sense

CCCAGCACAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCA
GAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAGTTTCAACAAGATAT
CATTGGGAAAGGAGGCGCAAACATTAAAAAGATTTCGTGAAGAAAGCAACACCAAAATCGACCTTCCAGCAGAGAA
TAGCAATTCCAGAGACCATTATCATCACAGGCAAGCGAGCCAAGTGCAGAGCTGCCCGG

SEQ ID NO:488

>GL3_43A1_2_M13F Direction: sense

CCCAGGACAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCA
GAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTGCTGTTCCGATCTTCAAACAGTTTCAACAAGAA
TATCATTGGGAAAGGAGGCGCAAACGATTCAAGAAAGATTTCGTGAAGAAAGCAACACCAAAATCGACCTTCCAGC
AGAGAATAGCAATTTCCAGAGACCATTATCAGTCACAGGCAAGCGAGCCAAGTGCAGAGGGTTGCCCTGGTCCGCT
AGAAACCCAGCACAGGTGGTTAGATGGATAACAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTTCACTGACTA
GTCGTTAAGGGCGAATTCCAGCACACTGGCGGCCGCTCGACTAGTGGATCCGAGCTC

SEQ ID NO:489

>GL3_43A1_2_M13R Direction: anti-sense

CCGGGCAGCTTCGCAGTTGGCTCGCTTGCCTGTGATGATAATGGTCTCTGAATTGCTATTCTCTGCTGGAAGGTC
GATTTTGGTGTGTGCTTTCTTCACGAATCTTTTAAATGTTTGCGCCCTCCTTTCCCAATGATATTCTTGTGAAACTG
TTTGAAGATCGGAACAGAAATTGAATAGCTATTTTCCACCAGATCTGCCACCATCTTCTGCATGTATTTTGTGCA
TTTTTCCACCTCATTCTTAGGTCCTCTGAGCTGGACAATGTCACTTTTTTGTGCTGGG

SEQ ID NO:490

>GL3_43A1_4_M13F Direction: sense

CCCAGCACAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCA
GAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAGTTTCAACAAGATAT
CATTGGGAAAGGAGGCGCAAACATTAAAAAGATTTCGTGAAGAAAGCAACACCAAAATCGACCTTCCAGCAGAGAA
TAGCAATTCCAGAGACCATTATCATCACAGGCAAGCGAGCCAAGTGCAGAGTTGCCCGGCCGAGAAACCCAGCAC
AGTGGTTAGATAGATAAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTCACTGACTGTCGTAAGGGCGAATTC
CAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGT

SEQ ID NO:491

>GL3_43A1_4_M13R Direction: anti-sense

CCGGGCAGCTTCGCAGTTGGCTCGCTTGCCTGTGATGATAATGGTCTCTGAATTGCTATTCTCTGCTGGAAGGTC
GATTTTGGTGTGTGCTTTCTTCACGAATCTTTTAAATGTTTGCGCCCTCCTTTCCCAATGATATTCTTGTGAAACTG
TTTGAAGATCGGAACAGAAATTGAATAGCTATTTTCCACCAGATCTGCCACCATCTTCTGCATGTATTTTGTGCA
TTTTTCCACCTCATTCTTAGGTCCTCTGAGCTGGACAATGTCACTTTTTTGTGCTGGG

SEQ ID NO:492

>GL3_43A_PCR_G3F1 Direction: sense

CCCAGCACAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCA
GAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAGTTTCAACAAGATAT
CATTGGGAAAGGAGGCGCAAACATTAAAAAGATTTCGTGAAGAAAGCAACACCAAAATCGACCTTCCAGCAGAGAA
TAGCAAGTTCAGAGACCATTATCATCACAGGCAAGCGAGCCAAGTGCAGAGCTGCCCGG

SEQ ID NO:493

>gi|4885408|ref|NM_005336.1| Homo sapiens high density lipoprotein binding protein (vigilin) (HDLBP), mRNA

GAATTCGGGGGGCGAGTAAGCCAGCGGCAGGACCAGCGGGCGGGGGCCACAACAAAAGCTGGCAGGCTGA
CAGAGGCGGCCCTCAGGACGGACCTTCTGGCTACTGACCGTTTTGCTGTGGTTTTCCCGATTGTGTGTAG
GTGTGAGATCAACCATGAGTTCGGTTGCAGTTTTGACCCAAGAGAGTTTTGCTGAACACCGAAGTGGGCT
GGTCCGCAACAAATCAAAGTTGCCACTCTAAATTCAGAAGAGGAGAGCGACCTCCAACCTACAAGGAT
GCCTTCCCTCCACTTCTTGAGAAAGCTGCTTGCCTGGAAAGTGCCAGGAACCCGCTGGAGCCTGGGGGA
ACAAGATCCGACCCATCAAGGCTTCTGTCACTCAGGTGTTCATGTACCCCTGGAGGAGAGAAAATA
CAAGGATATGAACCAAGTTTGGAGAAGGTGAACAAGCAAAAATCTGCCTTGAGATCATGCAGAGAACTGGT
GCTCACTTGGAGCTGTCTTTGGCCAAAGACCAAGGCCTCTCCATCATGGTGTGAGAAAGCTGGATGCTG
TCATGAAAGCTCGGAAGGACATTGTTGCTAGACTGCAGACTCAGGCCTCAGCAACTGTTGCCATTCCCAA
AGAACACCATCGCTTTGTTATTGGCAAAAATGGAGAGAACTGCAAGACTTGGAGCTAAAAACTGCAACC
AAAATCCAGATCCCACGCCAGATGACCCAGCAATCAGATCAAGATCACTGGCACCAAGAGGGCATCG

AGAAAAGCTCGCCATGAAGTCTTACTCATCTCTGCCGAGCAGGACAAACGTGCTGTGGAGAGGCTAGAAGT
AGAAAAGGCATTCCACCCCTTCATCGCTGGGCCGTATAATAGACTGGTTGGCGAGATCATGCAGGAGACA
GGCACGCGCATCAACATCCCCCACCAGCGTGAACCGGACAGAGATTGTCTTCACTGGAGAGAAGGAAC
AGTTGGCTCAGGCTGTGGCTCGCATCAAGAAGATTTATGAGGAGAAGAAAAAGAACTACAACCATTGC
5 AGTGAAGTGAAGAAATCCCAACACAAGTATGTCATTGGGCCCAAGGGCAATTCATTGCAGGAGATCCTT
GAGAGAACTGGAGTTTCCGTTGAGATCCCACCCTCAGACAGCATCTCTGAGACTGTAATACTTCGAGGCG
AACCTGAAAAGTTAGGTCAGGCGTTGACTGAAGTCTATGCCAAGGCCAATAGCTTCACCGTCTCCTCTGT
CGCCGCCCTTCTCTGGCTTCACCGTTTCATCATTGGCAAGAAAGGGCAGAACCTGGCCAAAATCACTCAG
CAGATGCCAAAGGTTACATCGAGTTACAGAGGGCGAAGACAAGATCACCTGGAGGGCCCTACAGAGG
10 ATGTCAATGTGGCCCAGGAACAGATAGAAGGCATGGTCAAAGATTTGATTAAACCGGATGGACTATGTGGA
GATCAACATCGACCACAAGTTCCACAGGCACCTCATTGGGAAGAGCGGTGCCAACATAAACAGAATCAAA
GACCAGTACAAGGTGTCCGTGCGCATCCCTCCTGACAGTGAGAAGAGCAATTTGATCCGCATCGAGGGGG
ACCCACAGGGCGTGCAGCAGGCCAAGCGAGAGCTGCTGGAGCTTGATCTCGCATGGAAAATGAGCGTAC
CAAGGATCTAATCATTGAGCAAAGATTTTCATCGACAATCATTGGGCAGAAGGGTGAACGGATCCGTGAA
15 ATTCGTGACAAAATCCCAGAGGTCATCATTAACTTTCCAGACCCAGCACAAAAAGTGACATTGTCCAGC
TCAGAGGACCTAAGAAATGAGGTGGAAAAATGCACAAAATACATGCAGAAGATGGTGGCAGATCTGGTGG
AAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAGTTTCACAAGAATATCATTGGGAAAGGAGGCGCA
AACATTTAAAAAGATTCGTGAAGAAAGCAACACCAAATCGACCTTCAGCAGAGAATAGCAATTCAGAGA
CCATTATCATCACAGGCAAGCGAGCCAACTGCGAAGCTGCCCGGAGCAGGATTCTGTCTATTTCAGAAAGA
20 CTTGGCCAAACATAGCCGAGGTAGAGGTCTCCATCCCTGCCAAGCTGCACAACTCCCTCATTGGCACCAG
GGCCGTCTGATCCGCTCCATCATGGAGGAGTGCGGCGGGGTCCACATTCACTTTCCCGTGGAAAGGTTTCAG
GAAGCGACACCGTTGTTATCAGGGGCCCTTCTCGGATGTGGAGAAGGCCAAGAAGCAGCTCCTGCATCT
GGCGGAGGAGAAGCAAACCAAGAGTTTCACTGTTGACATCCGCGCCAAGCCAGAATACCACAAATTCCTC
ATCGGCAAGGGGGGCGGCAAATTCGAAGGTGCGCGACAGCACTGGAGCACGTGTCATCTTCCCTGCGG
25 CTGAGGACAAGGACCAGGACCTGATCACCATCATTGGAAAGGAGGACGCCGTCCGAGAGGCACAGAAGGA
GCTGGAGGCTTGATCCAAAACCTGGATAATGTGTGGGAAGACTCCATGCTGGTGGACCCCAAGCACCAC
CGCCACTTCGTCATCCGAGAGGCCAGGTCTTGGGGAGATTGCTGAAGAGTATGGCGGGGTGATGGTCA
GCTTCCCACGCTCTGGCACACAGAGCGACAAAGTCAACCTCAAGGGCGCCAAGGACTGTGTGGAGGCAGC
CAAGAAACGCATTTCAGGAGATCATTGAGGACCTGGAAGCTCAGGTGACATTAGAATGTGCTATACCCAG
30 AAATTCATCGATCTGTCTATGGGCCCCAAAGGTTCCAGAATCCAGCAGATTACTCGGGATTTCAGTGTTC
AAATTAAATTCCCAGACAGAGAGGAGAACGCAGTTTCAGATACAGAGCCAGTTGTCCAGGAGAATGGGGA
CGAAGCTGGGGAGGGGAGAGAGGCTAAAGATTGTGACCCCGGCTCTCCAAGGAGGTGTGACATCATCATC
ATCTCTGGCCGGAAGAAAAGTGTGAGGCTGCCAAGGAAGCTCTGGAGGCATTGGTTCTGTCAACCATTG
AAGTAGAGGTGCCCTTTGACCTTCACCGTTACGTTATTGGGCAGAAAGGAAGTGGGATCCGCAAGATGAT
35 GGATGAGTTTGAGGTGAACATACATGTCCCGCACCTGAGCTGCAGTCTGACATCATCGCCATCACGGGC
CTCGCTGCAAAATTTGGACCCGGGCCAAGGCTGGACTGCTGGAGCGTGTGAAGGAGCTACAGGCCGAGCAGG
AGGACCGGGCTTTAAGGAGTTTAAAGCTGAGTGTCACTGTAGACCCCAAATACCATCCCAAGATTATCGG
GAGAAAGGGGGCAGTAATTACCCAAATCCGGTTGGAGCATGACGTGAACATCCAGTTTCTTGATAAGGAC
GATGGGAACCCAGCCCCAGGACCAATTACCATCACAGGGTACGAAAAGAACACAGAAGCTGCCAGGGATG
40 CTATACTGAGAATTGTGGGTGAACCTTGAGCAGATGGTTTCTGAGGACGTCCCGCTGGACCACCGCGTTCA
CGCCCGCATCATTGGTGGCCGCGGCCAAAGCCATTTCGCAAAATCATGGACGAATTCAAGGTGGACATTTCG
TTCCACAGAGCGGAGCCCCAGACCCCAACTGCGTCACTGTGACGGGGCTCCAGAGAATGTGGAGGAAG
CCATCGACCACATCTCAATCTGGAGGAGGAATACCTAGCTGACGTGGTGGACAGTGAGGCGCTGCAGGT
ATACATGAACACCCAGCACACGAAGAGGCCAAGGCACCTTCCAGAGGCTTTGTGGTGGCGGACGCACCC
45 TGGACCGCCAGCAGCAGTGAAGAGGCTCCTGACATGAGCAGCTCTGAGGAATTTCCAGCTTTGGGGCTC
AGGTGGCTCCCAAGACCTTCCCTTGGGGCCCCAAACGATAATGATCAAAAAGAACAGAACCCTCTCCAGC
CTGCTGACCCGAACCCAACACACAATGGTTTGTCTCAATCTGACCCAGCGGCTGGACCCTCCGTAAATT
GTTGAGCGCTCTTCCCTTCCCGAGGTCCGACGGGAGCCTAGCGCTGGCTGTGTGTGCGGCCGCTCCTC
CAGGCCTGGCCGTGCCCCGCTCAGGACCTGCTCCACTGTTTAACAATAAACCAAGGTCATGAGCATTTCGAG
50 CTAAGATAACAGACTCCAGCTCCTGGTCCACCCGGCATGTCAGTCAGCACTCTGGCCTTCATCACGAGAG
CTCCGAGCCGTGGCTAGGATTCCACTTCCGTGTGTCATGACCTCAGGAAATAAACGTCCTTGACTTTATA
AAAGCCCCGAATTC

SEQ ID NO:494

55 >gi|4885409|ref|NP_005327.1| high density lipoprotein binding protein;
vigilin [Homo sapiens]
MSSVAVLTQESFAEHRSGLVPPQIKVATLNSSEESDPPTYKDAFPPLPEKAACLESQAQEPAGAWGNKIRP
IKASVITQVFHVPLEERKYKDMNQFGEGEQAKICLEIMQRTGAHLELSLAKDQGLSIMVSGKLDAMVKAR
KDIVARLQTOASATVAIPKEHHRFVIGKNGEKLQDLELKTATKIQIPRPDDPSNQIKITGTKEGIEKARH
60 EVLLISAEQDKRAVERLEVEKAFHPFIAGPYNRLVGEIMQETGTRINIPPSVNRTEIVFTGEGEQLAQA
VARIKKIYEEKKKKTTTIAVEVKKSQHKYVIGPKGNSLQEIERTGVSVEIPPSDSISETVILRGEPEKL

GQALTEVYAKANSFTVSSVAAPSWLHRFIIGKKGQNLAKITQQMPKVHIEFTEGEDKITLEGPTEDVNVA
 QEQIEGMVKDLINRMDYVEINIDHKFHRHLIGKSGANINRIKDQYKVSVRIPPDSEKSNLIRIEGDPQGV
 QQAKRELLELASRMENERTKDLIIIEQRFHRTIIGQKGERIREIRDKFPEVIINFPDPAQKSDIVQLRGP
 NEVEKCTKYMQKQMVADLVENSYSISVPIFKQFHKNIGKGGANIKKIREESNTKIDLPAENSNSETIIIT
 5 GKRANCEAARSRLSIQKDLANIAEVEVSIPAKLHNSLIGTKGRILRSIMEECGGVHIHFPVEGSGSDTV
 VIRGPSSDVEKAKKQLLHLAEKQTKSFTVDIRAKPEYHKFLIGKGGGKIRKVRDSTGARVIFPAAEDKD
 QDLITIIIGKEDAVREAQKELEALIQNLNDNVVEDSMLVDPKHHRHFVIRRGQVLREIAEEYGGVMVSFPRS
 GTQSDKVTCLKGAKDCVEAAKKRIQEIIEDLEAQVTLECAIPQKFHRSVMGPKGSRIQQITRDFSVQIKFP
 10 DREENAVHSTEPVVQENGDEAGEGREAKDCDPGSPRRCDIIISGRKEKCEAAKEALEALVPVTIEVEVP
 FDLHRYVIGQKSGGIRKMMDEFVNIVHPAPELQSDIIAITGLAANLDRAKAGLLERVKELQAEQEDRAL
 RSFKLSVTVPKYHPKIIIGRKGAIVITQIRLEHDVNIQFPDKDDGNQPDQITITGYEKNTEAARDAILRI
 VGELEQMVSEDVPLDHRVHARIIGARGKAIRKIMDEFKVDIRFPQSGAPDPNCVTVTGLPENVEEAIDHI
 LNLEEEYLADVVDSEALQVYMKPPAHEEAKAPSRGFVVRDAPWTASSEKAPDMSSEEFPSFGAQVAPK
 TLPWGPKR

SEQ ID NO:495

Vimentin

>G3_8_04_PCR_G3F1 Direction: N/A

GCGGTCCAGGCCATCGCCACCCTCCGCAGCCATGTCCACCAGGTCCGTGTCCTCGTCTCCTACCGCAGATGTTT
 20 GCGCGCCCGGGCACCAGCGAGCCGGGCGGAGCTCCAGCCGGAGCTACGTGACTACGTCCACCCGCACCTACAGCCT
 GGGCAGCGCGCTGCGCCCCAGCACCAGCGCAGCCTCTACGCCTCGTCCCCGGGCGGCGTGTATGCCACGCGCTCC
 TCTGCCGTGCGCCTGCGGAGCAGCGTCCCCGGGGTGGCGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGAC
 GCCATCAACACCGAGTTCAAGAACACCCGCACCAACAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCA
 CTATATCGACAGGTGCGCTTCTTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAA
 25 GGCAAGTCGCGCTGGGGGACCTCTACGAGGAGGAGATGCGGGAGCTGCGCCGGC

SEQ ID NO:496

>gi|4507894|ref|NM_003380.1| Homo sapiens vimentin (VIM), mRNA

GGGCGCGCCAGAGACGCGAGCCGCGCTCCCACCAACCCACCCACCGCGCCCTCGTTCGCCTCTTCTCCGG
 30 GAGCCAGTCCGCGCCACCAGCGCCCGCCAGGCCATCGCCACCCTCCGCGAGCCATGTCCACAGGTCCGTG
 TCCTCGTCTCCTACCGCAGGATGTTGGCGGGCCCGGGCACCAGCGAGCCGCGGAGCTCCAGCGGAGCT
 ACGTGACTACGTCCACCCGCACCTACAGCCTGGGCAGCGCGCTGCGCCCCAGCACCAGCCGCGAGCCTCTA
 CGCCTCGTCCCCGGGCGGCGTGTATGCCACGCGCTCCTCTGCGCTGCGCCTGCGGAGCAGCGTGCCCGGG
 35 GTGCGGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGACGCCATCAACACCGAGTTCAAGAACACCC
 GCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTACATCGACAAGGTGCGCTT
 CCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAAGGCAAGTCGCGCCTA
 GGGGACCTCTACGAGGAGGAGATGCGCGAGCTGCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCC
 GCGTCGAGGTGGAGCGCGACAACCTGGCCGAGGACATCATGCGCCTCCGGGAGAAATTGCAGGAGGAGAT
 40 GCTTCAGAGAGAGGAAGCCGAAAACACCCTGCAATCTTTAGACAGGATGTTGACAAATGCGTCTCTGGCA
 CGTCTTGACCTTGAACGCAAAGTGAATCTTTGCAAGAAGAGATTGCCTTTTTGAAGAACTCCACGAAG
 AGGAAATCCAGGAGCTGCAGGCTCAGATTAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCC
 TGACCTCACGCTGCGCTGCGTGACGTACGTAGCAATATGAAAGTGTGGCTGCCAAGAACCCTGCAGGAG
 GCAGAAGAATGGTACAAATCCAAGTTTGCTGACCTCTCTGAGGCTGCCAACCAGCAATGACGCCCTGC
 45 GCCAGGCAAGCAGGAGTCCACTGAGTACCGGAGACAGGTGCAGTCCCTCACCTGTGAAGTGGATGCCCT
 TAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATGGAAGAGAACTTTGCCGTTGAAGCTGCT
 AACTACCAAGACACTATTGGCCGCTGAGGATGAGATTGAGAAATATGAAGGAGGAAATGGCTCGTCACC
 TTCTGTAATACCAAGACCTGCTCAATGTTAAGATGGCCCTTGACATTGAGATTGCCACCTACAGGAAGCT
 GCTGGAAGGCGAGGAGAGCAGGATTTCTCTGCCTCTTCCAAACTTTTCTCCCTGAACCTGAGGGAAACT
 50 AATCTGGATTCACTCCCTCTGGTTGATACCCACTCAAAAAGGACATTCCTGATTAAAGACGGTTGAAACTA
 GAGATGGACAGGTATCAACGAAACTTCTCAGCATCAGATGACCTTGAATAAAAAATTGCACACACTCAG
 TGGCAGGCGATATATTACCCAGGCAAGAATAAAAAAGAAATCCCATATCTTAAAGAAACAGCTTTCAAGT
 GCCTTTCTGCAGTTTTTTCAGGAGCGCAAGATAGATTTGGAATAGGAATAAGCTCTAGTTCTTAACAACCG
 ACATCCTACAAGATTTAGAAAAAGTTTACAACATAATCTAGTTTACAGAAAAATCTTGTGCTAGAATA
 55 CTTTTTAAAGGTATTTTGAATACCATTAATAACTGCTTTTTTTTTTCCAGCAAGTATCCAACCAACTTGG
 TTCTGCTTCAATAAATCTTTGGAAAACCTCCA

SEQ ID NO:497

>gi|4507895|ref|NP_003371.1| vimentin [Homo sapiens]

MSTRSVSSSSYRRMFGPGTASRPSSSSSYVTTSTRYSLSALRPSTSRSLYASSPGGVYATRSSAVRL
 60 RSSVPVGRLLQDSVDFSLADAINTEFKNTRTNEKVELQELNDRFANYIDKVRFLQQNKILLAELEQLKG

QGKSRLGDLYEEMRELRRQVDQLTNDKARVEVERDNLAEDIMRLREKLQEEMLQREEAENTLQSFQDV
DNASLARLDLERKVESLQEEIAFLKKLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQYESVA
AKNLQEAEEWYKSKFADLSEAANRNNDALRQAKQESTERYRQVQSLTCEVDALKGTNESLERQMREMEEN
FAVEAANYQDTIGRLQDEIQNMKEEMARHLREYQDLLNVKMALDIEIATYRKLEGEESRISLPLPNFSS
LNLRETNLDSLPLVDTHSKRTFLIKTVETRDGQVINETSQHDDLE

SEQ ID NO:498

>gi|22054529|ref|XM_167414.2| Homo sapiens vimentin (VIM), mRNA
GCCAGAGACGCAGCCGCGCTCCACCACCCACCCACCGCGCCCTCGTTCGCCTCTTCTCCGGGAGCCA
GTCCGCGCCACCGCCGCGCCGCCAGGCCATCGCCACCCCTCCGCAGCCATGTCCACCAGGTCCGTGTCTCG
TCCTCCTACCGCAGGATGTTTCGGCGGCGCCGGGCACCGCGAGCCGGCCGAGCTCCAGCCGGAGCTACGTGA
CTACGTCCACCCGCACCTACAGCCTGGGCGAGCGCGCTGCGCCCCAGCACCAGCCGAGCCTCTACGCCTC
GTCCCCGGGCGGCGTGTATGCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCAGCGTGCCCGGGGTGCGG
CTCCTGCAGGACTCGGTGGACTTCTCGTGGCCGACGCCATCAACACCGAGTTCAAGAACACCCGCACCA
ACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTACATCGACAAGGTGCGCTTCCTGGA
GCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAAGGCAAGTCGCGCCTGGGGGAC
CTCTACGAGGAGGAGATGCGGGAGCTGCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCCGCGTCG
AGGTGGAGCGCGACAACCTGGCCGAGGACATCATGCGCCTCCGGGAGAAATTGCAGGAGGAGATGCTTCA
GAGAGAGGAAGCCGAAAACACCCCTGCAATCTTTTCAGACAGGATGTTGACAATGCGTCTCTGGCAGCTCTT
GACCTTGAACGCAAGTGGAATCTTTGCAAGAAGAGATTGCTTTTTTGAAGAACTCCACGAAGAGGAAA
TCCAGGAGCTGCAGGCTCAGATTTCAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCCTGACCT
CACGGCTGCCCTGCGTGACGTACGTACGTCAGCAATATGAAAGTGTGGCTGCCAAGAACCTGCAGGAGGCAGAA
GAATGGTACAAATCCAAGTTTGTGACCTCTCTGAGGCTGCCAACCAGGAACAATGACGCCCTGCGCCAGG
CAAAGCAGGAGTCCACTGAGTACCGGAGACAGGTGCAGTCCCTCACCTGTGAAGTGGATGCCCTTAAAGG
AACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATGGAAGAGAACTTTGCCGTTGAAGCTGCTAAC'TAC
CAAGACACTATTGGCCGCTGCAGGATGAGATTGAGAATATGAAGGAGGAAATGGCTCGTCACCTTCGTG
AATACCAAGACCTGCTCAATGTTAAGATGGCCCTTGACATTGAGATTGCCACCTACAGGAAGCTGCTGGA
AGGCGAGGAGAGCAGGATTTCTGCGCTCTTCCAACTTTTCTCCTGAACTGAGGGAACTAATCTG
GATTCACCTCCCTCTGGTTGATACCCACTCAAAAAGGACACTTCTGATTAAAGACGGTTGAACTAGAGATG
GACAGGTTATCAACGAACTTCTCAGCATCACGATGACCTTGAATAAAAAATTGCACACACTCAGTGCAGC
AATATATTACCAGCAAGAATAAAAAAGAAATCCATATCTTAAAGAAACAGCTTTCAAGTGCCTTTCTGCA
GTTTTTTCAGGAGCGCAAGATAGATTTGGAATAGGAATAAGCTCTAGTTCTTAACAACCGACACTCCTACA
AGATTTAGAAAAAAGTTTACAACATAATCTAGTTTACAGAAAAATCTTGTGCTAGAATACTTTTTTAAAG
GTATTTTGAATACCATTAAACTGCTTTTTTTTTTCCAGCAAGTATCCAACCAACTTGGTTCTGCTTCAA
TAAATCTTTGAAAAAATC

SEQ ID NO:499

>gi|20473667|ref|XP_167414.1| similar to Vimentin [Homo sapiens]
MSTRSVSSSSYRRMFGGPGTASRPSSRSYVTTSTRYSLGSALRPSTSRSLYASSPGGVYATRSSAVRL
RSSVPGVRLQLQDSVDFSLADAINTEFKNTRTNEKVELQELNDRFANYIDKVRFLQONKILLAELEQLKG
QGKSRLGDLYEEMRELRRQVDQLTNDKARVEVERDNLAEDIMRLREKLQEEMLQREEAENTLQSFQDV
DNASLARLDLERKVESLQEEIAFLKKLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQYESVA
AKNLQEAEEWYKSKFADLSEAANRNNDALRQAKQESTERYRQVQSLTCEVDALKGTNESLERQMREMEEN
FAVEAANYQDTIGRLQDEIQNMKEEMARHLREYQDLLNVKMALDIEIATYRKLEGEESRISLPLPNFSS
LNLRETNLDSLPLVDTHSKRTLLIKTVETRDGQVINETSQHDDLE

SEQ ID NO:500

Vinexin (SCAM-1)

>GL3_37D_3_M13F Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGTCGATGGGGTGACAGGTGTGGACTGTCATGCATGC
AGTGTGACGACTGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCTAGAAATTTCGGAACGTTCCCTGGGAAATTACG
TTGCCCCGGTGTGAGTCGGTCTCCATGGCAACTTGAGAGCCAGCCAGGACTGGGGCTGGGNGAGCCGTGCTGGAC
AACTTCGCTAGGGAGGAGACGACGTGAACCACCCGGGCCACATTCTCCTTTCCCGCAGAGAACNCTTGAACGCT
CCCAGTAGTCTTGCCAGAAGCGGGAACGCACCACGGCCAGCCCATATTTACGCTCGGAGCCNCCCACCCACCTT
CGAAAGGCCCTTCCACTGGTAACATTGACTTCTCCAACCCCTACGGAAGGCTACAACAAGGGGGCCGATTTTCCG
CTTTCTCCCAACAGCCTCGCCTTGTGTTCNATTTTTCCCTTGCCTCCCAGACCCGAAATTTCCCNCGCGA
AAAATTACGAGAGGGGTCTTGGCCTATTTGAAAGGCNNGGCGAGNACCCTAATTTTCCAGCGCCCTGTNAT
TTTGAGNAACCCACGGAAA

SEQ ID NO:501

>GL3_37D_4_M13F Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGCG
ACGATGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
ACCCCCGCCACATCCCCTTCCCAGGACCTGAGCTCCCAGCATCTGCAGACGACCCACGGCAGACCTTTCCCTC
GGGAACCACACACTCGAAAGNCCCCCTGGGACTGAGTTCCCAAACAGGACTCACAGGGCAGTTCCCGTCCG
CAACGAGGTCCCGTTTTTCAACTTTGTCTTCNCCCAACACACCGAACATCCCCAAGAAGTACCAGGGAGGTCC
TGCATNTTGAAGCCGGGAGAACACNAGTTTATCCAGGGGCCGTATAATTNGAGGANA

SEQ ID NO:502

>GL3_15J_4_M13R Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGTTG
ACGATGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
ACCCCCGCCACATCCTCCTTCCCAGGACCTGAGCTCCCAGCATCTGCAGAACTGAAAACCCCCCGGGCAAGGG
CCCCTTTTCCCCCTTCGGGGGGAACCCCNACCACATACAGGNAAAGANAACCCATGNGAACAGGAAAACCCAAA
ACGANGAAAAAAGNGGAATACAACCAAAAAGAA

SEQ ID NO:503

>GL3_15J_3_M13R Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGTTG
ACGATGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
ACCCCCGCCACATCCTCCTTCCCAGGACCTGAGCTCCCAGCATCTGCAGACGANCCCCGAGCCTTTCCCTCGG
ACCACACACACTACGAAAGNNCACCCACAGGACCGGAGAACCAACAAAAGAAACGTCAACAGGGGCAAGTATAC
ACG

SEQ ID NO:504

>GL3_37D_2_M13F Direction: N/A

CACTATAGGGCGAATTGGGCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCC
CTTCTCTCGGCATGGACGAGCTGTACAAGGAGGAGGCCGCAAGGCCGTTGGCAGCGGTGGCTCCAGTGTGCTGG
GTTCTTGGCGCTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTGG
GGAGTGGGGTGGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCTGGGTGGGAATCAGTCCAGGGG
GCTTCGAGGGGGGTCCGAGGGAAAGGCTGCGGGGGGTCTGACTGCAGATGCTGGGAGCTCAGGTCTGGGGAAGG
AGGATGTTGGGCGGGGTCCTCTCCCTCCCACGAGTGCCACCGTCCCCACCATCCTGGCTGGCTCCAAGTTTGC
CATGGAGACCACTCACACCGGGGCAACGTAATTTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGAACA
CCCACAAAACAGCATCGTTTCACTGCTGCAATGACATCACACCTGTCCCTTCGCGCAGCTCCAAGCTCGTACT
TACGTTCTGGGGCCCTTGTACTTGGGTCCGGGCAGAAACCCAGCACAAAGATGGGGTTAAGAANTAGGAATTAA
AAAGGCGCGGGCCGGCATCCGAACCATAAANACATGGAAAGGGGACCTGAATAACNCAAACCTTGGAACTGGATCN
GNGACAAAGGGCGGCCGAAAATNTATCCCCAGCGNCCAACAACNATGGAGACGGGGCCCGGTACCAAAGATG

SEQ ID NO:505

>GL3_37D_1_M13F Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGTTG
ACGATGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
ACCCCCGCCACATCCTCCTTCCCAGGACCTGAGCTCCCAGCATCTGCAGACGAACCCCGCAGCCTTTCCCTCG
GAACCTCGAAGCGGAGAAAACAAGAAAAAGGAAAAAGGACCCATANTAANAATAA

SEQ ID NO:506

>GL3_15J_1_M13F Direction: N/A

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTGTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGCTGCAGATNCTGGGAGCTCAGGTCTTGGGGAAGGAGGATGTGGGCG
GGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCATCCTGGCTGGCTCCAAGTTGCCATGGAGACCACT
CACACCGGGCAACGTAATTTCCAGGGAACGTTCCGAATT

SEQ ID NO:507

>GL3_15J_1_M13R Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGTG
ACGATGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
5 ACCCCCGCCACATCCTCCTTCCCCAGGACCTGAGCTCCCAGCATCTGCAGACGACCCCCGAGCCTTCCCTCG
GACCCCCCTCGAAGCCCCCTGGACTGATTCCCACCACGATC

SEQ ID NO:508

>GL3_15J_2_M13F Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGT
10 GACGATGGCTGGTTTGTGGGTGTCTCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCG
GTGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAG
GACCCCCGCCACATCCTCCTTCCCCAGGACCTGAGCTCCCAGCATCTGCAGACGACCCCCGAGCCTTCCCTC
GGACCCTCGAA

SEQ ID NO:509

>GL3_15J_2_M13R Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGCAGATGCTGGGAGCTCAGGTCTTGGGGAAGGAGGATGTGGGCG
20 GGGTCTCTTCCCTCCCACGAGTGCCACCGCTCCCCACCCCATCTGGCTGGCTCCAAGTTGCCATGGAGACCAC
TCACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTTCCGGGAGACACCCACAAACCAGCC
ATCGTCACACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGCTCCAGCTCGTCTTCGTTCTGGGGCCTGTA
CTGGT

SEQ ID NO:510

>GL3_15J_3_M13F Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGCAGATGCTGGGAGCTCAGGTCTTGGGGAAGGAGGATGTGGGCG
30 GGGTCTCTTCCCTCCCACGAGTGC

SEQ ID NO:511

>GL3_15J_4_M13F Direction: N/A

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
35 GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGCAGATGCTGGGAGCTCAGGTCTTGGGGAAGGAGGATGTGGGCG
GGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCCATCTGGCTGGCTCCAAGTTGCCATGGAGACCACT
CACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTTCCGGGAGACACCCACAAACCAGCCA
40 TCGTCACAC

SEQ ID NO:512

>GL3_15J_PCR_G3F1 Direction: N/A

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
45 GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGCAGATGCTGGGAGCTCAGTCTTGGGGAAGGAGGATGTGGGCGG
GGGTCTCTCCCTCCCACAGTGCCACGTCACCGTCCCCACCCCATCTGGCTGGCTCCAAGTTGCCAGTGGAAGAAC
ACTCACCACCCGGGGCCAACCGGTAATTTCCAAGGGAACCGGTTCCCGAAATTTCTGGGGTCTTCCGGGAAAA
AACCAACAAAACAAGCCCTACGGCA

SEQ ID NO:513

>GL3_37B_PCR_G3F1 Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
55 GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGCAGATGCTGGGAGCTCAGTCTTGGGGAAGGAGGATGTGGGCGG
GGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCCATCTGGCTGGCTCCAAGTTGCCATGGAGACCACT
CACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTTCCGGGAGACACCCACAAACCAGCCA
TCGTACACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGCTCCGCTCGTCTTCGTTCTGGGGCCTGTACT
GGT

SEQ ID NO:514

>GL3_37D_1_M13R Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGAGATGCTGGGAGCTCAGGTCTGGGGAAGGAGGATGTGGGCG
GGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCATCCTGGCTGGCTCCAAGTTGCCATGGAGACCACTC
ACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCCAT
CGTCACACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGCTCCAGCTCGTCTCGTTCTGGGGCCTGTACT
GGTCCGCAGAAAACCCAGCACAGTGGTTAGATACGATAAAGCGGACCGCTCGACTAGTCTGAGGTCTGATACTCA
ACTGGACTGTGTAATGGGGCGAATTCTTGGCAAGATTTCCATCACACTTGCGGGGCGTCAAGCATGCAT

SEQ ID NO:515

>GL3_37D_2_M13R Direction: anti-sense

ACCATACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGACAGGGTGGATGTCATGCAGCAGTGTG
ACGATGGCTGGTTTGTGGGTGTCTCCCGAGGAGCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCGCG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
ACCCCGCCACATTCTCCTTTCCCGAGACCTGAGCTCCAGCATCTGCAGACGAACCCCGGAAGCTTCCCTCG
GA

SEQ ID NO:516

>GL3_37D_3_M13R Direction: N/A

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTTCAAAGCAGACCTCTTGTATTTGGGGAGTGGG
GTGGAGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGATCGGTGGGTGGGAATCAGTCCAGGGGGCTT
CGAGGGGGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGAGATCCTGGGAGCCTCAGGTCTGGGGAAGGAGGAT
GTGGGCGGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCATCCTGGCTGGCTCCAAGTTGCCATGG
AGACCACTCACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGAACCCACA
AACCAGCCATCGTCACACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGCTCCAGCTCGTCTCCGTNCTG
GGCCTGTACTGGTC

SEQ ID NO:517

>GL3_37D_4_M13R Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGAGATCCTTGGGAGCTCAGGTCTGGGGAAGGGGGATGTGGGC
GGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCAACCCATCCTGGCTGGCTCCAAGTTGCCATGGAGACCAC
TCACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCC
ATCGTCGCATGCTGCATGACATCCACCCTGTTCCCTCGCGCAGTTCAGCTCGTCTTACGTTCTGGGGCCTGT
AACTGGGT

SEQ ID NO:518

>GL3_37D_PCR_G3F1 Direction: sense

GCTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGG
TGGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGAGATCCTTGGGAGCTCAGGTCTGGGGAAGGGGGATGTGGGCG
GGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCATCCTGGCTGGCTCCAAGTTGCCATGAACCACTCA
CACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCCATC
GTCACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGCTCCGCTCGTCTTCGTTCTGGGGCCTGTACTGG
TCCGCAAAACCCAGCACAGTGGTTAGATGATTAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTCACTGACTTT
TTAA

SEQ ID NO:519

>gi|19923334|ref|NM_005775.2| Homo sapiens vinexin beta (SH3-containing adaptor molecule-1) (SCAM-1), mRNA

CGGACGCGTGGGCAGGCAGCAGCCGGGAGGATGCTCTCGCTCCCGGGCGGCCTCGGGCCCAGCCAC
CTGCTCGCCGGGGAAGAGGACACGCAGAGGAGCAGCTGGCTTGCCCGAGTCCTCCACCTTGACCCAAG
CATGCAGGGCCCACCCCGCAGCCTCCGCGTGGGCTCAGCCTGGACGACTTCATCCCTGGCCACCTCCAG
TCCCACATAGGGTCTTCTCCCGGGGACACGGGTGCCCGTGATCCGGAATGGTGGCTCCAACACCCCTTA
ATTTCCAGTTCCACGACCCCCGCGCCAGGACTGTGTGCAATGGGGGCTACACACCAAGACGAGATGCTTC
CCAGCACCCGGACCCTGCGTGGTATCAGACCTGGCCAGGCCCTGGGAGCAAGCCCTCTGCAAGCACAAAG
ATCCCTGCCTCCAGCACACCCAGAACTGGTCAGCCACGTGGACCAAGGACAGCAAGCGTCGGGACAAGC

GCTGGGTCAAGTACGAGGGAATCGGGCCCCGTGGACGAGAGCGGCATGCCCATTTGCCCCCGATCCAGCGT
 TGACAGACCCAGAGACTGGTACCGGAGAATGTTCCAGCAGATTACCGGAAAATGCCAGACTTGACAGCTG
 GACTGGACCTTCGAGGAGCCACCCAGAGACCCAGGCATCTAGGAGCCAGCAAAGACTGCCACACAGGC
 CCGGCCCCGGCAACATCTTCCAGTGAAGAAGCTGGGACCACCTCTGAAGAGTTACCTAGAAGCACCTCAA
 5 CTACAGACCTGGAGCATTCTCCACTGTGCTGCAGCCCTCAAATCAGGTGCTCAGACGCCGGGAAAAAGTA
 GACAATGTCTGGACGGAAGAGTCTTGAACCACTTTCTGCAGGAAGTAGAGACTGGGCAGAGGCCCAAGA
 AACCGCTGGTGGACGACCCTGGTGAGAAGCCCTCCAGCCCATTTAGAGTGTGCTGGAGAGAGAGCTGGC
 CGAGCTGAGCGCCGAGCTGGACAAGGACCTGCGGGCAATTGAGACCCGACTGCCGTCCCCAAGAGCTCG
 10 CCGGCGCCCCGACGGGCCCCGGAGCAGCGCCCCGGCCGGCCCGGCTCAGCCTGGAGCTCCAGCTACC
 CACATGCACCTTACCTGGGTTCCGCCCCGGTCCCTGAGTCCCCACAAAATGGCTGATGGAGGAAGCCCCCT
 CCTAGGTCGGAGGGACTTTGTCTACCTTCCCTCAACCCGAGACCCCTAGTGCCTCTAACGGAGGGGGCAGC
 CCAGCCAGGAGGGAAGAGAAGAAGAGAAAGGCCGCCAGGCTCAAGTTTGACTTCCAGGCGCAGTCCCCCA
 AGGAGCTGACTCTGCAGAAGGGTGACATTGTCTACATCCACAAGGAGGTGGACAAGAAGTGGCTGGAGGG
 15 AGAGCACCACGGCCGCTGGGCATCTTCCCTGCTAATTATGTGGAGGTGCTGCCCGCAGATGAGATCCCT
 AAGCCCATCAAGCCCCGACCTACCAGGTGCTGGAGTATGGAGAGGCTGTGGCCAGTACACCTTCAAGG
 GGGACCTGGAGGTGGAGCTGTCTTCCGCAAGGGAGAGCACATCTGCCTGATCCGCAAGGTGAACGAGAA
 CTGGTACGAGGGACGCATCAGGGCAGGGGCGCAAGGCATATTCCCTGCCAGCTACGTGCAGGTGTCT
 CGTGAACCCCGCTCCGGCTCTGTGACGACGGCCCCAGCTCCCCACGTCTCCCCGCTGACCGCTGCCG
 20 CCGCTCAGCCCGTACCCAGCTCCCCCTCAGCCCTCGCGAGCCAGCTGACCCACCGACTTGGGGGG
 ACAGACCTCCCCCGTGCAGCTGGCTTCTCTTCCCCACCCAGGAGCCTAGACCCAGACCCAGAATCTT
 GGCACCCCTGGTCCAGCTCTGTCCACTCTCGAGGTCCAGCCATCCCTTGGACCTGGGGACCTCCTCTC
 CTAACACCTCTCAGATACACTGGACCCGTAACGGGCGATGTACAGTACAGGCCCCAGAAGACGACGA
 GCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTATGCAGCAGTGTGACGATGGCTGGTTTGTGGGTGTC
 TCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCGGCTGTGAGTGGTCTCCATGG
 25 CAATTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGGACCCCCGCCACA
 TCCTCTTCCCCAGGACCTGAGCTCCAGCATCTGCAGACGACCCCCGAGCATTTCCTCGGACCCCCC
 TCGAAGCCCCCTGGACTGATTCCCAACCCAGCATCACAGGCATTCTCCACAGCCCTTTTCAATTTCTCTC
 CCACCCACTCCCCAAATACAGAGGTCTGCTTTGAAGCGGAGACCATTTCCAGGCCTTATTGAGACCAGA
 CCCCAGTCCCCACCCCATCTGCTCCAGCGTTTCTCTAACAGGGACAGCTCTCCGCTTTGCCCCC
 30 ACGGGTCTCTAACCAGAACAGCTTCTAGCCTCGTAGAGACCAAAGGCCGCCCGCTGCTGGGG
 TTCCTCCCAGCACCCAGCTTGTGCTGCCCTCTTTGCCTTCTGGCCTCCAGCTGGGTGTGGGGGGCG
 GAGCAAGGCGGGGGACAGACGACACCTTCTTAGCGATCTAGGCCTGGCAAGAGCTCTGGCCCCAAGGC
 CTCTCTTCCAGGGGCTGCCAAGTCTGGCCCTGGCCCTGGCATATCACCCGCACTGTGGGGCCAGGC
 35 ACCACTAGCCTGGCTCAAATATTTCCCAAGGAGACTGCTGTGTGCTGCCCGCTGCCTGCTGGCTCTCCC
 CCAGCCCCACATCCCTCTGGAAGAGAATGTAAATAAACCTGGACACAAGGGCCTTCGTGGCCTCGA

SEQ ID NO:520

>gi|19923335|ref|NP_005766.2| vinexin beta (SH3-containing adaptor
 molecule-1) [Homo sapiens]
 40 MQGPPRSLRAGLSLDDFIPGHLQSHIGSSSRGTRVPVIRNGGSNTLNFQFHDPAVRTVCNGGYTPRRDAS
 QHPDPAWYQTPGPGSKPSASTKIPASQHTQNSATWTKDSKRRDKRWVKYEGIGPVDESGMPIAPRSSV
 DRPRDWYRRMFQQIHRKMPDLQLDWTFEPPRPRLHGAQQRPAHRPGPATSSSGRSWDHSEELPRSTFN
 YRPGAFSTVLQPSNQVLRREKVDNVWTEESWNQFLQLELTGQRPKPLVDDPGEKPSQPIEVLLERELA
 45 ELSAELDKDLRAIETRLPSPKSSPAPRRAPQRPPAGPASAWSSSYPHAPYLGSARSLSPHKMADGGSPF
 LGRDRFVYPSSTRDPSASNGGSPARREEKKRKAARLKFDFOAQSPKELTLQKGDIVYIHKEVDKNWLEG
 EHHGRLGIFPANYVEVLPADDEIPKPIKPPTYQVLEYGEAVAQYTFKGDLEVELSFRKGEHICLIRKVNEN
 WYEGRITGTGRQGIFFASYVQVSREPRRLRLCDDGPQLPTSPRLTAAARSARHPSSPSALRSPADPTDLGG
 QTSRRTGFSFPTQEP RPQTQNLGTPGPALSHSRGPSHPLDLGTSSPNTSQIHWTPYRAMYQYRPQNEDE
 50 LELREGDRVDVMQCCDDGWFGVSRRTQKFGTFPGNYVAPV

SEQ ID NO: 521

NM_004265 (Homo sapiens fatty acid desaturase 2 (FADS2))NM_004265.2
 GI:14141180

1 agggggcgcg gtgggaggag taggagaaga caaaagccga aagcgaagag ggccccgggct
 55 61 gcacacaccg gctgggaggc agccgtctgt gcagcgagca gccggcgcg ggaggccgca
 121 gtgcacgggg cgacacagtc ggcaggcagc atggggaagg gagggaaacca gggcgagggg
 181 gccgcgcagc gcgaggtgtc ggtgccacc ttcagctggg aggagattca gaagcataac
 241 ctgcgcaccg acaggtggct ggtcattgac cgcaaggttt acaacatcac caaatggtcc
 301 atccagcacc cggggggcca cggggtcatc gggcactacg ctggagaaga tgcaacggat
 60 361 gccttcgcgc ccttcacccc tgacctgga ttcgtgggca agttcttgaa acccctgctg
 421 attggtgaac tggccccgga ggagcccagc caggaccacg gcaagaactc aaagatcact

5 481 gaggacttcc gggccctgag gaagacggct gaggacatga acctgttcaa gaccaaccac
 541 gtgtttcttc tctctctcct ggccacacatc atcgccctgg agagcattgc atgggttact
 601 gtcttttact ttggcaatgg ctggattcct accctcatca cggcctttgt ccttgctacc
 661 tctcaggccc aagctggatg gctgcaacat gattatggcc acctgtctgt ctacagaaaa
 721 cccaagtgga accaccttgt ccacaaattc gtcattggcc acttaaagggt tgcctctgcc
 781 aactgggtgga atcatcgcca cttccagcac cacgccaagc ctaacatctt ccacaaggat
 841 cccgatgtga acatgctgca cgtgtttgtt ctgggccaat ggcagcccat cgagtacggc
 901 aagaagaagc tgaaatacct gccctacaat caccagcacg aatacttctt cctgattggg
 961 ccgcgcgtgc tcatccccat gtatttccag taccagatca tcatgacct gatcgtccat
 10 1021 aagaactggg ttggacctggc ctgggcccgc agctactaca tccggttctt catcacctac
 1081 atccctttct acggcatcct gggagccctc cttttcctca acttcatcag gttcctggag
 1141 agccactggg ttgtgtgggt cacacagatg aatcacatcg tcatggagat tgaccaggag
 1201 gcctaccgtg actggttcag tagccagctg acagccacct gcaacgtgga gcagtccttc
 1261 ttcaacgact ggttcagtgg acaccttaac ttccagattg agcaccacct cttccccacc
 15 1321 atgccccggc acaacttaca caagatcgcc ccgctgggtga agtctctatg tgccaagcat
 1381 ggcattgaat accaggagaa gccgctactg agggccctgc tggacatcat caggtccttg
 1441 aagaagtctg ggaagctgtg gctggacgcc taccttcaca aatgaagcca cagcccccg
 1501 gacaccgtg ggaaggggtg caggtggggg gatggccaga ggaatgatgg gcttttgttc
 1561 tgaggggtgt ccgagaggct ggtgtatgca ctgctcacgg acccatggtt ggatctttct
 20 1621 ccctttctcc tctccttttt ctcttcacat ctccccata gcacctgccc ctcatgggac
 1681 ctgccctccc tcagccgtca gccatcagcc atggccctcc cagtgcctcc tagccccctc
 1741 ttccaaggag cagagaggtg gccaccgggg gtggctctgt cctacctcca ctctctgccc
 1801 ctaaagatgg gaggagacca gcggtccatg ggtctggcct gtgagtctcc ccttgagcc
 1861 tggctactag gcatcacccc cgctttgggt cttcagatgc tcttgggggt cataggggca
 25 1921 ggtcctagtc gggcagggcc cctgaccctc ccggcctggc ttcactctcc ctgacggctg
 1981 ccattgggtcc accctttcat agagaggcct gctttgttac aaagctcggg tctccctcct
 2041 gcagctcggg taagtaccg aggcctctct taagatgtcc agggccccag gccgcggggc
 2101 acagccagcc caaaccttgg gccctggaag agtccctcac cccatcacta gactgtctctg
 2161 accctgggct ttcacggggc ccattccacc gcctccccaa cttgagcctg tgaccttggg
 30 2221 accaaagggg gagtccctcg tctcttgtga ctcagcagag gcagtggcca cgttcaggga
 2281 ggggcccggc ggcctggagg ctcagccac cctccagctt ttccctcagg tgctccagga
 2341 tccaagattc tggagcaatc tgacccttct ccaaaggctc tgttatcagc tgggcagtgc
 2401 cagccaatcc ctggccattt ggccccaggg gacgtggggc ctgcaggctg caggagggca
 2461 ctggagctgg gaggtctcgt cccagccctc cccatctcgg ggctgctgtg tggacggcgc
 35 2521 tgcctcaggc actctcctgt ctgaacctgc ccttactgtg tttaacctgt tgctccagga
 2581 tgcatctctga taggaggggg cggcagggtc gggccttgtg acaatctgcc tttcaccaca
 2641 tggccttgcc tcggtggccc tgactgtcag ggagggccag ggagggcag cggaggggag
 2701 tctcaggagg aggctgccct gaggggctgg ggagggggta cctcatgagg accagggtgg
 2761 agctgagaag aggaggaggt gggggctgga ggtgctggta gctgagggga cgggcaagtg
 40 2821 agaggggagg gaggaagtc ctgggaggat cctgagctgc tgttgagtc taaccacta
 2881 atcagttctt agattcagg gaagggcagg caccaacaac tcagaatggg ggctttcggg
 2941 gagggcgccct agtcccccca gctctaagca gccaggaggg acctgcatct aagcatctgg
 3001 gttgccatgg caatggcatg cccccagct actgtatgcc cccgaccccc gcagaggcag
 3061 aatgaacca tagggagctg atcgtaatgt ttatcatggt acttccccac ccctacattt
 45 3121 tttgaaataa aataaggaat tttattctc

SEQ ID NO:522

NP_004256 (fatty acid desaturase 2; linoleoyl-CoA desaturase (delta-6-desaturase)-like 2; delta-6 fatty acid desaturase) [Homo sapiens].NP_004256.1 GI:4758334

50 1 mgkggnqgeg aaerevsvpt fsweeiqkhn lrtdrwlvid rkvnitkws iqhpggqrvi
 61 ghyagedatd afrafhpdle fvgkflkpl1 igelapeeps qdhgknskit edfralrkta
 121 edmnlfktnh vfflllllahi ialesiawft vfyfgngwip tltitafvlat sqaqagwlqh
 55 181 dyghlsvyrk pkwnhlvkhf vighlkgasa nwnnhrhfqh hakpnifhkd pdvnmlhvf
 241 lgewqpieyg kklklylpyn hqheyyfflig ppllipyf yqiimtmivh knwvdlawav
 301 syirffity ipfygilgal lflnfirfle shwfvwtqm nhivmeidqe ayrdwffssql
 361 tatcnveqsf fndwfsghln fqiehhlfpt mprhnlhkia plvkslcakh gieyqekpl1
 421 ralldiirsl kksghklwlda ylhk

SEQ ID NO:523

AF134404 (Homo sapiens delta-6 fatty acid desaturase (CYB5RP) mRNA),
AF134404.1 GI:4868365

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5      1 cttcgcttcc ctcggggtct tgctcggacc tcggccaccg cctgggatcc ccaggactcg
      61 tgcgtgcagc atgggcggcg tcggggagcc gggaccgcgg gagggacccg cgcagccggg
      121 ggcaccgctg cccaccttct gctgggagca gatccgcgcg cacgaccagc cgcgcgacaa
      181 gtggctgggtc atcgagcgcc gcgtctacga catcagccgc tgggcacagc ggcaccagg
      241 gggcagccgc ctcatcgccc accacggcgc tgaggacgcc acggatgcct tccgtgcctt
      301 ccatcaagat ctcaattttg tgcgcaagtt cctacagccc ctggtgattg gagagctggc
10     361 tccggaagaa cccagccagg atggaccctt gaatgcgcag ctggtcgagg acttccgagc
      421 cctgcaccag gcagccgagg acatgaagct gtttgatgcc agtcccacct tctttgcttt
      481 cctactgggc cacatcctgg ccatggaggt gctggcctgg ctccctatct acctcctggg
      541 tcctggctgg gtgcccagtg ccctggccgc ctccatcttc aagaagtcct ggtggaacca
15     601 ctggtgtctg cagcatgacc tgggccatgc ctccatcttc aagaagtcct ggtggaacca
      661 cgtggcccag aagttcgtga tggggcagct aaagggttcc tccgcccact ggtggaactt
      721 ccgccacttc cagcaccacg ccaagcccaa catcttccac aaagaccagc acgtgacggt
      781 ggcgcccgtc ttcctcctgg gggagtcata cgtcgagtat ggcaagaaga aacgcagata
      841 cctaccctac aaccagcagc acctgtactt ctccctgatc ggcccgcgcg tgctcaccct
20     901 ggtgaacttt gaagtggaaa atctggcgta catgctgggtg tgcattgagc gggcggtatt
      961 gctctgggccc gccagcttct atgcccgtt ctctctatcc tacctcccct tctacggcgt
     1021 ccctgggggtg ctgctcttct ttgttgctgt cagggtcctg gaaagccact ggttcgtgtg
     1081 gatcacacag atgaaccaca tccccaggga gatcggccac gagaagcacc gggactgggt
     1141 cagctctcag ctggcagcca cctgcaacgt ggagccctca cttttacca actggttcag
25     1201 cgggcacctc aacttccaga tcgagcacca cctcttcccc aggatgccga gacacaacta
     1261 cagccgggtg gccccgctgg tcaagtcgct gtgtgccaag cacggcctca gctacgaagt
     1321 gaagcccttc ctcaccgcgc tgggtggacat cgtcaggtcc ctgaagaagt ctggtgacat
     1381 ctggctggac gcctacctcc atcagtgaag gcaacaccca ggcgggcaga gaagggtca
30     1441 gggcaccagc aaccaagcca gccccggcg ggatcgatac cccacccct ccactggcca
     1501 gcctgggggt gcactgcctg ccctcctggt actgttgtct tcccctcggc cccctcacat
     1561 gtgtattcag cagccctatg gccttggtc tgggcctgat gggacagggg tagagggag
     1621 gtgagcatag cacattttcc tagagcgaga attgggggaa agctgttatt tttatattaa
     1681 aatacattca gatgtaaaaa aaaaa

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SEQ ID NO:524

35 AAD31282 (delta-6 fatty acid desaturase) [Homo sapiens]. AAD31282.1
GI:4868366

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      1 mggvgepgpr egpaqpgapl ptfcweqira hdqpgdkwlv ierrydydisr waqrhpqgsr
      61 lighhgaeda tdafrafhqd lnfvrkflqp lligelapee psqdgplnaq lvedfralhq
40     121 aaedmklfda sptffafllg hilamevlaw lliyllpggw vpsalaafil aisqaqswcl
      181 qhdlghasif kkswnnhvaq kfvmgqlkgf sahwwnfrhf qhhakpnifh kdpdvtvapv
      241 flgessvey gkkkrrylpy nqghlyffli gpplltlvnf evenlaymlv cmqwadllwa
      301 asfyarffls ylpfygvpv llffvavrvi eshwfwwitq mnhipkeigh ekhrdwvssq
      361 laatcnveps lftnwfsghl nfqiehhfip rmprhnysrv aplvkslcak hglseyevkpf
45     421 ltalvdivrs lkksgdiwld aylhq

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